

# FIGURE 1

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCTCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC  
TCCAGCAGCATCAGCAGCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGG  
AGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA  
AGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT  
TCTGGTGTGAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTTAGGGTGTGTGCT  
GTCCCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCTGTCAGCGTGTGTACCAGCCCTTCC  
TCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATTATAGGACCGCCTAC  
CGCCGAGCCCTGGGCTGGCCCCTGCCAGGCCTCGCTACGCGTGTGCCCCGGCTGGAAGAG  
GACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAG  
GGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG  
TCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGC  
CGGCAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG  
TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGACAGTGCAATGAAG  
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCT  
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC  
TCCTGGTGCACCTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTC  
CTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGG  
CTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTC  
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTTTTCTCCTC  
CCCTTCCCTCGGGAGGGTCCCCAGACCCTGGCATGGGATGGGCTGGGATTTTTTTTGTGAAT  
CCACCCCTGGCTACCCCCACCCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA  
GCTGAGGGAAGGTACGAGTTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC  
CGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAATGAAA  
CGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCT  
AGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGT  
TACAAAT

09978299 101504

## FIGURE 2

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV  
SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC  
GAAICQPPCRNGGSCVQPGRCRCPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCW  
EGHSLSADGTLCVPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLAS  
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKDS

### **Signal sequence:**

amino acids 1-19

### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 93-97, 270-274

### **N-myristoylation sites.**

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,  
191-197, 265-271

### **Amidation site.**

amino acids 26-30

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 152-164

### **Cell attachment sequence.**

amino acids 130-133

### **EGF-like domain cysteine pattern signature.**

amino acids 123-135

09978229.101501  
"05101" 55282660

# FIGURE 3

CGCTCGCCCCGTCGCCCCCTCGCCTCCCCGCAGAGTCCCCCTCGCGGCAGCAGATGTGTGTGGG  
 GTCAGCCACACGGCGGGGACTATGGTGAAATTCCCGGCGCTCACGCACTACTGGCCCCCTGATC  
 CGGTTCTTGGTGCCCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCTTGAA  
 CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT  
 ACTCCCTCATGAAGTTCTTCACGGGTCCCATGAGTGACTTCAAAAATGTGGGCCTGGTGT  
 GTGAACAGCAAGAGAGACAGGACCAAAGCCGTCTGTGTATGGTGGTGGCAGGGGCCATCGC  
 TGCCGTCTTTCACACACTGATAGCTTATAGTGATTTAGGATACTACATTATCAATAAACTGC  
 ACCATGTGGACGAGTCGGTGGGGAGCAAGACGAGAAGGGCCTTCCTGTACCTCGCCGCCTTT  
 CCTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAACACAAATACAGTTT  
 CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTTGTAGCCATTTTGC  
 TTCACAGTCACCTGGAATGCCGGGAGCCCCCTGCTCATCCCGATCCTCTCCTTGTACATGGGC  
 GCACTTGTGCGCTGCACCACCCTGTGCCTGGGCTACTACAAGAACATTACGACATCATCCC  
 TGACAGAAGTGGCCCCGAGCTGGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT  
 GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT  
 TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA  
 CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTTCG  
 ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCAGCCACATC  
 AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTTCGTGATGTTTTGGAC  
 ACCCAACGTGTCTGAGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC  
 TCTGTGTTGTTCTTTGCGGATCTTCTCCTTCTTCCAGTTCCAGTCACAGTGAGGGCGCAT  
 CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTCTTGGCCCCAGCTCTGTGCTGCG  
 GATCATCGTCTCATCGCCAGCCTCGTGGTCTTACCCTACCTGGGGGTGCACGGTGCACACC  
 TGGGCGTGGGCTCCCTCCTGGCGGGCTTTGTGGGAGAATCCACCATGGTTCGCCATCGCTGCG  
 TGCTATGTCTACCGGAAGCAGAAAAAGAGATGGAGAATGAGTCGGCCACGGAGGGGAAGA  
 CTCTGCCATGACAGACATGCCTCCGACAGAGGAGGTGACAGACATCGTGGAATGAGAGAGG  
 AGAATGAATAAGGCACGGGACGCCATGGGCACTGCAGGGACGGTCAGTCAGGATGACACTTC  
 GGCATCATCTCTTCCCTCTCCCATCGTATTTTGTTCCTTTTTTTTTTGTGTTTTGTTTGGTAAT  
 GAAAGAGGCCTTGATTTAAAGGTTTCGTGTCAATTCTCTAGCATACTGGGTATGCTCACACT  
 GACGGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTAAAAACAAACGAAACAACTGAC  
 TTCATACCCCTGCCTCACGAAAACCCAAAAGACACAGCTGCCTCACGGTTGACGTTGTGTCC  
 TCCTCCCCCTGGACAATCTCCTCTTGGAAACCAAAGGACTGCAGCTGTGCCATCGCGCCTCGGT  
 CACCCTGCACAGCAGGCCACAGACTCTCCTGTCCCCCTTCATCGCTCTTAAGAATCAACAGG  
 TTAAAACTCGGCTTCTTTGATTGTCTTCCAGTCACATGGCCGTACAAAGAGATGGAGCCC  
 CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGCAG  
 GAGGCGGGTGGCAGCTGCAGCCCGGAGTCCCCGTTCACTGAGGAACGGAGACCTGTGAC  
 CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAAATGCCCCGGG  
 GGCAGCAAACTGACATGGTTGAATGATAGCATTTCACTCTGCGTTCTCCTAGATCTGAGCAA  
 GCTGTGAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTTTTAAATTGTACAAAA  
 GCGCATCTCCAGATTCCAGACCCTGCCGCATGACTTTTCTGAAGGCTTGCTTTTCCCTCGC  
 CTTTCCTGAAGGTTCGATTAGAGCGAGTCACATGGAGCATCCTAACTTTGCATTTTAGTTTT  
 TACAGTGAAGTGAAGCTTTAAGTCTCATCCAGCATTCTAATGCCAGGTTGCTGTAGGGTAAC  
 TTTTGAAGTAGATATATTACCTGGTTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTAA  
 TTGAGAATGTACTACGGTACTTCCCTCCCACACCATACGATAAAGCAAGACATTTTATAACG  
 ATACCAGAGTCACTATGTGGTCTCCTCCCTGAAATAACGCATTTCGAAATCCATGCAGTGCAGTA  
 TATTTTTCTAAGTTTTTGGAAAGCAGGTTTTTCTTTAAAAAAATATAGACACGGTTCACT  
 AAATTGATTTAGTCAGAATTCCTAGACTGAAAGAACCTAAACAAAAAAATATTTTAAAGATA  
 TAAATATATGCTGTATATGTTATGTAATTTATTTAGGCTATAATACATTTCTATTTTCGC  
 ATTTTCAATAAAATGTCTCTAATAACAAAAA

09978299-101501

## FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF  
TGPMSDFKNVGLVFNNSKRDRTKAVLCMVVAGAIAAVFHTLIAYS DLGYYI INKLHHVDES  
GSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC  
REPLLIPILSLYMGALVRCTTLC LGYYKNIHDIIPDRSGPELG DATIRKMLSFWWPLALIL  
ATQRISRPIVNL FVSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN  
KLVSTSNVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAF AELCVVPLR  
IFSFFPVPVTVRAHLTGWMLTKKTFVLAPSSVLRIIVLIASLVVLPYLG VHGATLGVGSL  
AGFVGESTMVAIAACYVYRKQKKMENESATEGEDSAMTDMPPTEEVTDIVEMRENE

### **Transmembrane domains:**

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,  
408-423, 431-445

098294501  
TOSTOT" 66284660



## FIGURE 5

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT  
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT  
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA  
CCCTGTGGGTCACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTTCG  
ACAAGAATAACCCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCCACATC  
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC  
ACCCAACGTGTCTGNGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC  
TCTGTGTTGTTTCCTTTGCGGATCTTCTCCTTCTTCCCAGTTCAGTCACAGTGAGGGCGCAT  
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTC

0978299-101501  
TOSTOT 56284660

## FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG  
GAGCAGGGCAAAACAGTNACGGGCAGCCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC  
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTTGAT  
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTTCCTTTGCGGATTTTCT  
CCTTTTTCCCAGTTCCAGTCACAGNGAGGGCGCATCTCACCGGGNGGNTGATGACANTGAAG  
AAAACCTTTGTCCTTGCCCCCAGCTNNTTTGGTGCGGATCATTTGTCCTNATNGCCAGCCTTGT  
GGTCCTACCCTACCTGGGGGTGCACGGTGCGACCCTGGGCGTGGGTTCCCTCCTGGCGGGCA

09978269.101501  
F05F0F 66287660

## FIGURE 7

TATTCCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGACACTGAAGAAA  
ACCTTNGTCCTTGCCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT  
CCTACCCTACCTGGGGGTGCACGGTGAGAC

09978229.101501  
FOSTOT" 66282660

## FIGURE 8

GCCCCGCGCCCGGCGCCGGGCGCCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGA  
 GCCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG  
 CTGCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCCTCTTCC  
 TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGAGAGTCAGCTCTACAAGCTG  
 CCCTGGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGG  
 CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCT  
 TCTTTTTTACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG  
 AATGGGTTTTGGTTCTTTAAGTTCTTGATCCTGGTGGGCCTCACCGTGGGTGCCCTTCTACAT  
 CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCCTCTTCA  
 TCCTCATCCAGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC  
 AAGGCCGAGGAGTGCGATTCCCCTGCCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTT  
 CTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTTCATGTACTACACTGAGCCAGCGGCT  
 GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT  
 GCTGTCTTGCCCAAGGTCCAGGACGCCCAGCCAACTCGGGTCTGCTGCAGGCCTCGGTCTAT  
 CACCCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA  
 ACCCCCATTTGCCAACCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG  
 ACCCAGTGGTGGGATGCCCCGAGCATTGTGGGCCTCATCATCTTCCTCCTGTGCACCCTCTT  
 CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC  
 CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCC  
 TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCT  
 GGCTCACTGCACGTGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA  
 TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC  
 TACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTTGAGGCAGCCT  
 CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCT  
 GCCCCCTCCCCACACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTG  
 CCCCTGAGCCGGGCCTTCTAGTCGTAGTGCCCTCAGGGTCCGAGGAGCATCAGGCTCCTGCA  
 GAGCCCCATCCCCCGCCACACCCACACGGTGGAGCTGCCTCTTCCTTCCCCTCCTCCCTGT  
 TGCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGG  
 CTGCTGGAGAGAGCGGGGAACTCCACCACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTT  
 CCTGGTCACGTCCCCCAGGGGACCCTGCCCCCTTCTGGACTTCGTGCCTTACTGAGTCTCT  
 AAGACTTTTTCTAATAACAAGCCAGTGCGTGTAACAAAAA

T05101" 66284660

## FIGURE 9

MGACLGACSLLSASCCLCGSAPCILCSCCPASRNSTVSRIFTFFFLGVLVSIIMLSPGVE  
SPLYKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRD  
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSW  
NQRWLGKAEECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTF  
VCVSIAAVLPKVQDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA  
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA  
ACEGRAFDNEQDGVTSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVVKICAS  
WAGLLLYLWTLVAPLLLLRNDRFS

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

09976299-101501  
TDSFOT" 66291660

## FIGURE 10

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTCGAGCCCTCTGGCAGAGGGTTAACCTGGGTG  
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA  
AGTCCTGAGCGCTCAAGTTTGTCCGTAGGTGCGAGAGAAGGCCATGGAGGTGCCGCCACCGGC  
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCCGAGTCTTTGCTGCCGAAGCTG  
TGA CTGCCGATTTCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC  
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG  
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG  
TGTATGGGGGAATACCAGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA  
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT  
CATTCGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTTTGTGACTATATTCAACACAG  
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAATTGCAGGA  
GCTGTCACGGGAAGTCTTTTTAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCAT  
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTTCAGAAGTACGCTG  
GTGAGACTGTTTCAGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACTGGAA  
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG  
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACC  
CTTCAGTAATAGATAAACAAGACAAGGACTGAAAGTGCTCTGAACTTGAACTCACTGGAGA  
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC  
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGCTTTTTCTTTCTT  
TTTAACTAAGAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT  
TATGTTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA  
GCAGTAAATAAAACATTTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

0978299-10501

## FIGURE 11

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318

><subunit 1 of 1, 285 aa, 1 stop

><MW: 32190, pI: 9.03, NX(S/T): 2

MEVPPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF  
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAIEYHNRFDVQSAH  
RAATRGFIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSLFRINVGLR  
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELEWKGRLLQVTEHLPE  
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-24

#### **Transmembrane domains:**

amino acids 76-96 and 171-195

#### **N-glycosylation site:**

amino acids 153-156

09978299.101501  
T05T0T.66287660

## FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA  
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA  
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT  
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTCGTTCATG  
GCTGGCGCCGAACC

09978299 101501



## FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT  
TTTTCTGTAGAGCATTGTGCCTATTTCCCCGAGTTTTTGTCTGCCGAAGCTGTGACTGCCGAT  
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG  
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA  
ATACCAGCTTTTATTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA  
TAACC

0978299-104501  
TEST OF 65284660

## FIGURE 14

GAGCCGCCGCCGCGCGCGCGCGCGCACTGCAGCCCCAGGCCCGGCCCGGCCACCCACGTCT  
GCGTTGCTGCCCCGCCTGGGCCAGGCCCAAAGGCAAGGACAAAGCAGCTGTCAGGGAACCT  
CCGCCGGAGTCGAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGGTTTGCGGGG  
GCTTCGCGTGTTCCAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTG  
CTGCTAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT  
CGGCGTGGTCATTGCAGTGGGCATCTTCTTGTTTCTGATTGCTTTAGTGGGTCTGATTGGAG  
CTGTAAAACATCATCAGGTGTTGCTATTTTTTTATATGATTATTCTGTTACTTGTATTTATT  
GTTTCAGTTTTCTGTATCTTGCGCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT  
GGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT  
GTGGGTTCCGAAGTGTTAACCCTAAATGACACCTGTCTGGCTAGCTGTGTTAAAGTGACCAC  
TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTTGG  
TGGCATTGGCCTGTTCTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACA  
GGAACCAGAAAGACCCCCGCGCGAATCCTAGTGCATTCCTTTGATGAGAAAACAAGGAAGAT  
TTCCTTTCTGATTATGATCTTGTTCACTTTCTGTAATTTCTGTTAAGCTCCATTTGCCAGT  
TTAAGGAAGGAAACACTATCTGGAAAAGTACCTTATTGATAGTGGAATTATATATTTTTACT  
CTATGTTTCTCTACATGTTTTTTTCTTTCCGTTGCTGAAAAATATTTGAAACTTGTGGTCTC  
TGAAGCTCGGTGGCACCTGGAATTTACTGTATTCATTGTCTGGGCACTGTCCACTGTGGCCTT  
TCTTAGCATTTTTACCTGCAGAAAACTTTGTATGGTACCCTGTGTTGGTTATATGGTGAA  
TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCTAC  
TGGAAAAAGAGTGGAATTTATTAAATCAGAAAGTATGAGATCCTGTTATGTTAAGGGAAA  
TCCAAATTCCTAATTTTTTTTTGGTCTTTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTA  
TAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAAATAGTTAT  
GTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTGGTTT  
CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAAATGGAACGAGTTT  
TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAA  
AAGACTGCATTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGATATTTG  
ATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAATTTCTCAGTATTGTAACAGCAACTT  
GTCAAACCTAAGCATATTTGAATATGATCTCCCATATTTGAAATTGAAATCGTATTGTGTG  
GCTCTGTATATTCTGTAAAAAATTAAAGGACAGAAACCTTCTTTGTGTATGCATGTTTGA  
ATTAAAGAAAGTAATGGAAG

099899 10501

## FIGURE 15

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVGVVIAVGIFLFLIALV  
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLALNQEQQGQLLEVGNNTASARNDIQR  
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRFVGGIGLFFSFTEILGVWL  
TYRYRNQKDPRANPSAFL

### **Signal Peptide:**

amino acids 1-34

### **Transmembrane domains:**

amino acids 47-63, 72-95 and 162-182

09978299.101501  
TOSTOT " 66282660

## FIGURE 16

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTATATGATTATTCTGTAANT  
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG  
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT  
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCTAAATGACACCTGTNTGGCTAGCTGTGTTAA  
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA  
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC  
TACAGATACAGGAACCAG

09578299-101501

## FIGURE 17

AATCCCAAATTCCCAATTTTTTTGGNCTTTTATAGGGAAGATGTGTTGTGGTAAAAAGTGT  
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG  
TTATGTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG  
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG  
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG  
TCTAAAAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGAT  
ATTTGATTATCTTAAAAATTGTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC  
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT  
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC  
CCACTTGC

09978299.101501

## FIGURE 18

ATGATTATTCTGTTACTTGTATTTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTAGCCC  
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG  
TGACTCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGGTTCGGAAGTGTTAACCC  
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA  
TCATAGGAGAATATGC

09978299.101501

## FIGURE 19

CAGTCACCAATGAAGCTGGGCTGTGTCCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG  
 CTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGT  
 CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT  
 TCCAGGTCAAGGCCTACACTTTTCAGTGAACCCTTCCACCTGATTGTGTCTATGACTGGCTG  
 ATCCTCCAAGGTCCAGCCAAGCCAGTTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC  
 CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC  
 CCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC  
 TGCAGTGGCATCTTCCAGAGCCCTGGTCTGGGATCCCAGAAACAGCATCTGTTGTGGCTAT  
 CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG  
 CAGGAAGCCCCATGACCCTGAGTTGTGAGACAAAGTTGCCCCTGCAGAGGTGAGCTGCCCGC  
 CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT  
 CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCATACTGGTGTGAGGCAGCCACTGAGG  
 ACAACCAAGTTTGGAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT  
 GCTGCACCTCCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAAGTCTCCTGA  
 GGAGGCCCCCTGGGCCTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT  
 CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG  
 CAGGATGTGAGAGTCCTCCTCGGTACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA  
 GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAAGTAAACAGTTCATCCATGATCTCACT  
 TAACCACCCCAATAAATCTGATTCTTTATTTTCTTCTTCTGTCCTGCACATATGCATAAGTA  
 CTTTTACAAGTTGTCCCAGTGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAAATAAATTT  
 ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC  
 TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAA  
 CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACA  
 TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGGTGGGGGATGGTGGGATGT  
 GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG  
 GGCAGTACCCACACAACGAAAAATAATCTGGCCCAAATGTCAGTTGTACTGAGTTTGAGAAA  
 CCCCAGCCTAATGAAACCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT  
 TATCTCTTTCCAGCCTCATTCAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGCTATG  
 GTCTGTTCTTTAGTTCTAGTTTGTATCCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC  
 AAGGTGATGGCATTAAAGAAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC  
 ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCTTCCACCAT  
 ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTCGCCAAACACCG  
 ACTCTGTCTGTTGCCCTTGATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAAATTCTGG  
 TTGTTTGTAGCCTAA

09978299.101501

## FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594

><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV  
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCAWQDWPLTQVTFYRDGSALGPPGP  
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS  
PMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ  
VWKQSPQLEIRVQGASSAAPTTLNPAPQKSAAPGTAPEEAPGPLPPPPTPSSDPGFSSPL  
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

### **Signal sequence:**

amino acids 1-17

### **Leucine zipper pattern sequence:**

amino acids 12-33

### **Protein kinase C phosphorylation site:**

amino acids 353-355

0978299-101501  
TOSTOT" 55282560



## FIGURE 21

CCCACGCGTCCGCCCACGCGTCCGCCCACGGGTCCGCCCACGCGTCCGGGCCACCAGAAAGTT  
 TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG  
 ATCTTACTGGGCCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT  
 GGAAGTGCCAGAGAGTGTAACAGGACCTTGGAAGGGGATGTGAATCTTCCCTGCACCTATG  
 ACCCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCT  
 GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCG  
 CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCTGGAGATGG  
 ATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGATGGCAACCAAGTCGTG  
 AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCACAGTGACAAC  
 TGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC  
 GGGGTTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACCAGGAACCCATC  
 AAAGTAGCAACCCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA  
 TTTCTGCATGCCAAGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG  
 TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC  
 TTGAAAGCAACATCTACAGTGAAGCAGTCTGGGACTGGACCACTGACATGGATGGCTACCT  
 TGGAGAGACCAGTGCTGGGGCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT  
 CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTGCGAAGACATCCCAA  
 CAAGAGCATGTCTACGAAGCAGCCAGGTAAGAAAGTCTCTCCTCTTCCATTTTTGACCCCGT  
 CCCTGCCCTCAATTTTGTATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC  
 AATCCTAAGGCCGGAGGCCCTCAGGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT  
 CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC  
 AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA  
 AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA  
 TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT  
 CCAGTGATGAGCCAACTTCCCAGAATCTGGGCAACAACACTACTCTGATGAGCCCTGCATAGGA  
 CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCGCCTGCTGGACACAGTTCC  
 TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTTAAAAATGCCCCATTAGGC  
 CAGGATCTGCTGACATAATTGCCTAGTCAGTCCTTGCCTTCTGCATGGCCTTCTTCCCTGCT  
 ACCTCTCTTCCCTGGATAGCCCCAAAGTGTCCGCCTACCAACACTGGAGCCGCTGGGAGTCACT  
 GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTGGCTCTGG  
 GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG  
 CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA  
 CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT  
 TTCTCTTTCTTCAGGGCCAGACAGCTTTTAATTGAAATTGTTATTTACAGGCCAGGGTTCA  
 GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA  
 ATCATAACAGC

T05T01 " 66282550

## **FIGURE 22**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLLGHLLTVDTYGRPILEVPESVTGPWKGDVNLPTDYDPLQGYTQVLVKWLVQRGS  
DPVTIFLRDSSGDHIQQAKYQGRLVSHKVPDVSLLSTLEMDDRSYHTCEVTWQTPDGNQ  
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLSLQCQARGSPPISYIWKQQTNNQE  
PIKVATLSTLLFKPAVIADSGSYFCTAKQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMT  
YPLKATSTVKQSWDWTDDMDGYLGETSAGPGKSLPVFAIILIIISLCCMVVFTMAYIMLCRKT  
SQQEHVYEAAR

### **Signal Sequence:**

amino acids 1-19

### **Glycosaminoglycan attachment site:**

amino acids 149-152

### **Transmembrane domain:**

amino acids 282-300

09078299-101501  
TOSTOT 66282660

## FIGURE 23

GCGCCGGGAGCCCATCTGCCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT  
 GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTCCGA  
 GCGCCCGGCGCCCGCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC  
 GGGATGTCCTCTCCTCTTCTCCTCTTGCTAGTTTCCTACTATGTTGGAACCTTGGGGACTCA  
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC  
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA  
 GTGGTGATCACTTACTCCAGTCGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG  
 AGTGGCCTTTGCTTCCAATTTCTGCGAGGAGATGCCTCCTTGCGAGATTGAACCTCTGAAGC  
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTGAGGGCGCTACGTGTGGAGCCAT  
 GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC  
 AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCACTCTGGCACAGAGCCCATTGTGTATT  
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT  
 GACTACAACCACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTACTCTGGACTGTA  
 CCAGTGACACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGT  
 ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG  
 ATTTTCCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA  
 GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAGCCCGTCTTGTGAAACCCAGCT  
 CCTCTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCTCCACTCGCTCCACAGCAAAT  
 AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGCTGGCCAC  
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG  
 CTAATCTGACCAAAGCAGAAACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA  
 ACGGTCTGAATTACAATGGACTTGACTCCCACGCTTTCTAGGAGTCAGGGTCTTTGGACTC  
 TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA  
 GTGAGCATTGCACGGAACAGATTGAGATGAGCATTCTTCTTATAACAATACCAACAGCAA  
 AGGATGTAAGCTGATTGATCTGTAAAAAGGCATCTTATTGTGCCCTTTAGACCAGAGTAAGGG  
 AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG  
 AGGTGAATATACCTAAAACTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTCACAATT  
 TTCAAGAGGAAATGGGATGCTGTTTGTAATTTTCTATGCATTTCTGCAAACCTTATTGGATT  
 ATTAGTTATTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC  
 TGAGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC  
 TTCATTTGTCATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA  
 AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAAC  
 TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTCCATCTTCATGATGTT  
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTCCTCAAT  
 CAGATGCCTCTAAGGACTTTCCTGCTAGATATTTCTGGAAGGAGAAAATAACAACATGTCATT  
 TATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA  
 CCAACATACCATTAAGTCTCTTCTTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG  
 GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA  
 TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC  
 ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

09078299 101501

## FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLTDIEWLLTDNEGNQKV  
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV  
ILKVLVRPSKPKCELEGELTEGSDLTLOCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID  
YNHPGRVLLQNLTMSSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI  
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSSGSRSSSRGSSSTRSTANS  
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 232-251

09978299.101501

# FIGURE 25

GTCGTTCTTTGCTCTCTCGCGCCAGTCTCTCCCTGGTTCTCTCAGCCGCTGTCTGGAGGAGAGCACCCGGA  
 GACGCGGGCTGCAGTCGCGGCGGCTTCTCCCCGCTGGGCGGCTCGCCGCTGGGCAGGTGCTGAGCGCCCTAG  
 AGCCTCCCTTGCCTCCTCTCTGCGCGCCGAGCAGTGACATGGGGTGTGGAGGTAGATGGGCTCCCG  
 GCGCGGAGGCGGCGGTGGATGCGGCGCTGGGCAGAAAGCAGCCGCGATTCCAGCTGCCCCGCGCGCCCCGGGCG  
 CCCCTGCGAGTCCCCGGTTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCCGCTCGCCTCCTGAGCCGATC  
 GCCCCGCGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCTGCTTGGATTCTTAGCACCACCACAGCTCAG  
 CCAGAACAGAAGGCCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT  
 GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCT  
 GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCATGGCCAATG  
 ATTGAGAAATTACCTTGTGCTGCCCTTACTGACCGAGAAATGCACTTGCCACCTGGCATGTTCCAGTCTAACGCT  
 ACCTGTGCCCCCATACGGTGTGTCTGTGGGTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG  
 TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCTTCTAGTGTGATGAAATGCAAAGCATACACAGACTGT  
 CTGAGTCAGAACTGGTGGTGATCAAGCCGGGGACCAAGGAGACAGACAACGCTCTGTGGCACACTCCCGTCTTTC  
 TCCAGCTCCACCTCACCTTCCCCCTGGCACAGCCATCTTCCACGCCCTGAGCACATGGAAACCCATGAAGTCCCT  
 TCCTCCACTTATGTTCCCAAAGGCATGAACCTCAACAGAATCCAACCTTCTGCCTCTGTTAGACCAAAGGTACTG  
 AGTAGCATCCAGGAAGGGACAGTCCCTGACAAACACAAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAGACCCTC  
 CCAAACCTTCAGGTAGTCAACCACCAGCAAGGCCCCCACCACAGACACATCCTGAAGCTGCTGCCGTCCATGGAG  
 GCCACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAG  
 CATTTTGACATCAATGAGCATTTGCCCTGGATGATTTGCTTTTCTGCTGCTGGTGCTTGTGGTGATTGTGGTG  
 TGCAGTATCCGAAAAGCTCGAGGACTCTGAAAAAGGGGCCCCGGCAGGATCCAGTGCCATTGTGGAAGGGCA  
 GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT  
 ATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTTCTTTGCAATGCCAGTGAG  
 AGGGAGGTGCTGCTTTCTCAATGGGTACACAGCCGACCAGAGCGGGCTACGCAGCTCTGCAGCACTGGACC  
 ATCCGGGGCCCCGAGGCCAGCCTCGCCAGCTAATTAGCGCCCTGCGCCAGCACCCGAGAAACGATGTTGTGGAG  
 AAGATTCTGTGGGCTGATGGAAGACACCACCCAGCTGGAAACTGACAACTAGCTCTCCCGATGAGCCCCAGCCCG  
 CTTAGCCCCGAGCCCCATCCCCAGCCCCAACCGGAACTTGAGAATTCCGCTCTCCTGACGGTGGAGCCTTCCCCA  
 CAGGACAAGAACAGGGCTTCTTCGTGGATGAGTGGGAGCCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC  
 TCCGCGCTGAGCAGGAACGGTTCCTTTATTACCAAAGAAAAGAAGGACACAGTGTGCGGCAGGTACGCCCTGGAC  
 CCTGTGACTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTGAAGAG  
 ATTCCCCAGGCTGAGGACAACTAGACCGCTATTGAAATTATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC  
 CTCCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAACATAGGGATACTGCATTCTGGAAATTACTCA  
 ATTTAGTGGCAGGTGGTTTTTTAATTTTCTTCTGTTTCTGATTTTTGTTGTTTGGGGTGTGTGTGTGTGTGTGT  
 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT  
 TCTCTCTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCCTTTGCCAGGTGTAACGTGTGTGAA  
 ATACCCACCCTAAAGTTTTTTAAGTTCCATATTTTCTCCATTTTGCCCTTCTTATGTATTTTCAAGATTATTCTG  
 TGCATTTTAAATTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC  
 TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTACACCTACTTTTT  
 AAAAACAAAATATTATTACTATTTTTATTATTGTTTGTCTTTTATAAATTTTCTTAAAGATTAAAGAAAATTTAAGA  
 CCCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTTCATATTTCATGG  
 CTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTTACCTGGACACCGTGTAGAATGCTTGATTACTTGTAC  
 TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT  
 GACAACTGGGCCACCAAAGAACTTGAACCTTACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACCTT  
 GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGTCTTG  
 TTTTTATATACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCTGGTGGGATTCCTTCACCAATT  
 ACTTTAATTAAAAATGGCTGCAACTGTAAGAACCTTGTCTGATATATTTGCAACTATGCTCCCATTTACAAATG  
 TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTTGTGG  
 GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTTGTTA  
 AAAAAAAA

05976299-101501

## FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594

><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSPSSSTALASCSRIARRATATMIAGSLLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATG  
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMIEKLPCA  
ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKKGTETEDVRCKQCARGTFSDVPSSVMKC  
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP  
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHIL  
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIVVCSIRK  
SSRTLKKGPRQDPSAIVEKAGLKKSMPTQNRKWIYYCNGHGIDILKLVAQVGSQWKDIY  
QFLCNASEREVAAFSNGYTADHERAYAALQHWTIRGPEASLAQLISALRQHRNDVVEKIRG  
LMEDTTQLETDKLALPMSPSPSPSPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLL  
RCDSTSSGSSALSRNGSFITKEKDDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ  
AEDKLDRLFEEIGVKSQEASQTLTLLDSVYSHLPDLL

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 350-370

09978299-101501  
TOSTOT 66284660

## FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTTGGGA  
 CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC  
CATGGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCGGATCGCTTTTTTGGCC  
 TTGATGATTTGAAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG  
 TCACTGCTGCCATTGAAGTTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC  
 ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT  
 TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGGAGGAC  
 GAGTACCGCTGTGTCCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTTACAGCTGCTTC  
 GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCCAAC  
 TGGGTTTTCCCAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGAGTTC  
 CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA  
 CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCACTGCACAGCCT  
 GTGGTCATAGAAGGGGCTACAGCTCACGCATCGTGGGTGGAACATGTCCTTGCTCTCGCAG  
 TGGCCCTGGCAGGCCAGCCTTCAGTTCAGGGCTACCACCTGTGCGGGGGCTCTGTTCATCAC  
 GCCCCTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGA  
 CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCCTTGGTGGAGAAG  
 ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT  
 GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAAGAGA  
 ACTTCCCCGATGGAAAAGTGTGCTGGACGTCAGGATGGGGGGCCACAGAGGATGGAGGTGAC  
 GCCTCCCCTGTCTGAAACCACGCGGCCGTCCCTTTGATTTCACAAAGATCTGCAACCACAG  
 GGACGTGTACGTTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG  
 TGGACAGCTGCCAGGGGGACAGCGGGGGGCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG  
 TTAGTGGGAGCGACCAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC  
 CCGTGTACCTCCTTCCCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAA  
 GAGGAAGGGGACAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCGATCCTCCCCT  
 GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCTTGAGAGCTCTGAGTTCGGGCACCA  
 GTAGCAGGCCCCGAAAGAGGCACCCTTCCATCTGATTCCAGCACAACTTCAAGCTGCTTTTT  
 GTTTTTTGTTTTTTTGAGGTGGAGTCTCGCTCTGTTGCCAGGCTGGAGTGCAGTGGCGAAA  
 TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCCCTCAGCTTCCCCA  
 GTAGCTGGGACCACAGGTGCCCGCCACCACACCCAACTAATTTTTGTATTTTTAGTAGAGAC  
 AGGGTTTACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT  
 CAGCCTCCCACAGTGCTGGGATTACAGGCATGGGGCCACCACGCCTAGCCTCACGCTCCTTTC  
 TGATCTTCACTAAGAACAAAAGAAGCAGCAACTTGCAAGGGCGGCCTTTCCCACTGGTCCAT  
 CTGGTTTTTCTCTCCAGGGTCTTGCAAAATTCTTGACGAGATAAGCAGTTATGTGACCTCACG  
 TGCAAAGCCACCAACAGCCACTCAGAAAAGACGCACCAGCCAGAAAGTGCAGAACTGCAGTC  
 ACTGCACGTTTTTCATCTCTAGGGACCAGAACCAAACCCACCCTTTCTACTTCCAAGACTTAT  
 TTTCACATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAAGGCCTATTTTCATGATTTCTT  
 TGTAGCATTTGGTGCTTGACGTATTATTGTCCTTTGATTCCAATAATATGTTTCTTCCCT  
 CATTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAATCATCCACTGAAA

09978299-101501

## FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA  
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAAS  
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVLTALHH  
SVYVREGCASGHVVTLOCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT  
PLWIITAACVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL  
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAPLI SNKICNHR  
DVGGGIISPSMLCAGYLTGGVDSCQGDSSGGLVCQERRLWKLVGATSFQIGCAEVNKPQVYT  
RVTSFLDWIHEQMERDLKT

### **Signal Peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 240-284

097829-101501  
TOSTOT" 6628/660



# FIGURE 29

CCCACGCGTCCGTCTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTTATTGCAACGGTCAAGGCTGGCTTGT  
 GCCAGAACGGCGCGCGCGCGCACGACACACACGCGGGGAAACTTTTTTAAAAATGAAAGGCTAGAAGA  
 GCTCAGCGCGCGCGCGCGCGCTGCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTTCGCGA  
 CGCCCCGGCCCCGGCTCGGCGCCCCGCTGGGATGGTGCAGCGCTCGCCGCGGGCCGAGAGCTGCTGCACTGAAG  
 GCCGGCGACGATGGCAGCGCGCCCCGCTGCCCCGTGTCCCCCGCCCGCCCTCCTGCTCGCCCTGGCCGGTGTCT  
 GCTCGCGCCCTGCGAGGCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTGAGTGCCTCTGT  
 TCGGAGTGGGGACCTCTGGATCCAGTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGTGAATATTGCACT  
 ACAACGGGAAAGCAAAGAAGTATGATCATAAATCTGGAAAGAAATGAAGGTCTCATTGCCAGCAGTTTCACGGAAAC  
 CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGT  
 ACGGGGATATTCTGATTACAGCAGTCACTCTCAGCACGTGTTCTGGTCTCAGGGGACTTATTGTGTTTGAAAATGA  
 AAGCTATGTCTTAGAACCAATGAAAAGTGAACCAACAGATACAACTCTTCCAGCGAAGAAGCTGAAAAGCGT  
 CCGGGGATCATGTGGATCACATCACAACACCAAACCTCGCTGCAAAGAATGTGTTTCCACCACCCTCTCAGAC  
 ATGGGCAAGAAGGCATAAAAGAGAGACCCTCAAGGCAACTAAGTATGTGGAGCTGGTATCGTGGCAGACAACCG  
 AGAGTTTCAGAGGCAAGGAAAGATCTGGAAAAGTTAAGCAGCGATTAAATAGAGATTGCTAATCAGTTGACAA  
 GTTTTACAGACCACTGAACATTCCGATCGTGTGGTAGGCGTGGAAGTGTGGAATGACATGGACAAATGCTCTGT  
 AAGTCAGGACCCATTACCCAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAATCCCA  
 TGACAATGCGCAGCTTGTGAGTGGGGTTTATTTCCAAGGGACCACCATCGGCATGGCCCCAATCATGAGCATGTG  
 CACGGCAGACCAGTCTGGGGGAATTGTCTATGGACCATCAGACAATCCCCTTGGTGCAGCCGTGACCCTGGCACA  
 TGAGCTGGGCCACAATTTCCGGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA  
 AGGAGGCTGCATCATGAACGCTTCCACCAGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTT  
 GGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCTGTTTAACTGCGGAAGTCAGGGAGTCTTTCCGGGGCCA  
 GAAGTGTGGGAACAGATTTGTGGAAGAAGGAGAGGAGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG  
 CTGCAATGCCACCACCTGTACCTGAAGCCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT  
 GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCTGTGACCTCCAGAGTTCTGCACAGGGGCCAGCCC  
 TCACTGCCCCAGCCAATGTGTACCTGCACGATGGGCACTCATGTGAGGATGTGGACGGCTACTGCTACAATGGCAT  
 CTGCCAGACTCACGAGCAGCAGTGTGTACGCTCTGGGGACCAGGTGCTAAACCTGCCCCCTGGGATCTGCTTTGA  
 GAGAGTCAATTCTGCAGGTGATCCTTATGGCAACTGTGGCAAAGTCTCGAAGAGTTCTTTTGCCAAATGCGAGAT  
 GAGAGATGCTAAATGTGGAAAAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTC  
 CATAGAAAACAAACATCCCTCTGCAGCAAGGAGGCCGATTCTGTGCCGGGGGACCCACGTGTACTTGGGCGATGA  
 CATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTGCCTGAATCGTCAATGTCA  
 AAATATTAGTGTCTTTGGGGTTACGAGTGTGCAATGCAGTGCCACGGCAGAGGGGTGTGCAACAACAGGAAGAA  
 CTGCCACTGCGAGGCCCACTGGGCACCTCCCTTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCC  
 CATCCGGCAAGCAGAAGCAAGGCAGGAAGCTGCAGAGTCCAACAGGGAGCGCGGCCAGGGCCAGGAGCCCGTGGG  
 ATCGCAGGAGCATGCGTCTACTGCCTCACTGACACTCATCTGAGCCCTCCCATGACATGGAGACCCTGACCAGTG  
 CTGCTGCAGAGGAGGTACGCGTCCCCAAGGCCCTCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT  
 TCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAA  
 CAGTGCAAGGAAGGGCAGCGACTTCTGGTTGAGCTTCTGCTAAAACATGGACATGCTTCAGTGTCTCCTGAG  
 AGAGTAGCAGGTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTC  
 ACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCAGTGTCCCCCTTCCCCAGTGACACCTCAGCCT  
 TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTTATTATATGAAAA  
 AGCAGGGTTTTAGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATCTCCATCCAAGCAAACCTGAATGGCAA  
 TGAAACAACTGGAGAAGAAGGTAGGAGAAAGGGCGGTGAACTCTGGCTCTTTGCTGTGGACATGCGTGACCAGC  
 AGTACTCAGTTTGGGGTTTGCAGAAAGCCAGGGAACCCACAGAGTCACCAACCCTTCATTTAACAAGTAAGAA  
 TGTTAAAAAGTGAAAACAATGTAAGAGCCTAACTCCATCCCCCGTGGCCATTACTGCATAAAATAGAGTGCATT  
 GAAAT

66282650  
 TOSTOT

## FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVVSASVRSGLDWIPVKSFDK  
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCCYYHGHVRG  
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPKAKLKSVRGSCGSHHNTPNLA  
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGDLEKVKQRLIEIANHVDFK  
YRPLNIRIVLVGVEVWNDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG  
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFNGMNHDTLDRGCSCQMAVEK  
GGCIMNASTGYPPFPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEE  
CDCGEPEECMNRCCNATTCTLKPDAVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS  
PHCPANVYLHDGHSCQDVGVCYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGN  
CGKVS KSSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIETNIPLQQGGRILCRGTHVYLG  
DDMPDPGLVLGATKCADGKICLNRCQONISVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP  
FCDKFGFGGSTDSGP IRQAEARQEAAESNRERGGQGEVPGSQEHASTASLTII

**Signal peptide:**

amino acids 1-28

0978299.101501  
FOSTOT 66282660

## FIGURE 31

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA  
ACAAAACAGTTTTTGGGGGTT CAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA  
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG  
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA  
AGAGGACTCAAAAGTTTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT  
GGGCCCAGTGTCCTTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT  
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT  
AGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

09978299-101501  
TOSTOT" 66282660

## FIGURE 32

CATCCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTGTATTTTGGTAGAGATGGGA  
TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCCGCTCGGCCTCCC  
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAACTTTTAAAGAAGTTAAT  
GAAACCATACTTTTACATTTTAAATGACAGGAAAATGCTCACAATAATTGTTAACCCAAAA  
TTCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAATA  
TACCAAATATCAATAATACTTATCTCTGGGTAAAAACCTCTTCTCATACCCTGTGCTAACAA  
CTTTTAACAAAAAATTTGCATCACTTTTAAGAATCAAGAAAAATTTCTGAAGGTCATATGGG  
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTTCGAAATCTGCCT  
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTTGTTTCGA  
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCCCC  
TTGAATATAAGACCCTACTTGCTATCTCCCCTGCACCAGCCAGGAGCCACCCATCCTCCAGC  
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAAATGGGTAAGGGGATGGTGGCGA  
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTTCTTCATTTGTT  
CCTTTAACCAAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAACAGTGCCCT  
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAAGAGG  
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACTATAAACCGAATCCAATGGTGCCT  
AGAAGTTCAATGTGGCAAGGAAAAAAACCAGGTCTTCATCAAATCTACTAATTTCACTCCTT  
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT  
GACTAGATGATAAATGCCTGTACTCCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG  
AGGTCAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA  
AATATTGACTGGGCGTGGTGGTGAGTGCCTGTGATCCCAGCTACTCAGGTGGCTGAAGCAGG  
ACAATCACTTGAACCTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA  
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGCCAAGTGCAGTGGCT  
CACGCCTGTAATCCCGGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTGAGGAGATCA  
AGACCATCCTGGCTAATACAGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCCGGG  
GATGGTGGCAGGCACCTGGAGTCCCAGTACTCGGGAGGCTGAGGCAGGAGAATAGCGTGAA  
CTCAGGAGGCGGAGCTTGCAAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG  
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA

097829.101501

## FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVLLAL  
LHLYH

**Signal peptide:**

amino acids 15-27

TDSTOT" 6528/660

# FIGURE 34

GCCGCGGCGAGAGCGCGCCAGCCCCGCGCGATGCCCCGCGCGCCAGGACGCCTCCTCCCCGCTGCTGGCCCCGGC  
 CGGCGGCCCCGACTGCGCTGCTGCTGCTGCTGCTGGGCCATGGCGGCGGCGGGCGCTGGGGCGCCCGGGCCAGG  
 AGGCGGCGGCGGCGGCGGCGGACGGGCCCCCGCGGCAGACGGCGAGGACGGACAGGACCCGCACAGCAAGCACCC  
 TGTACACGGCCGACATGTTACCGCACGGGATCCAGAGCGCCGCGCACTTCGTATGTTCTTCGCGCCCTGGTGTG  
 GACACTGCCAGCGGCTGCAGCCGACTTGGAAATGACCTGGGAGACAAATACAACAGCATGGAAGATGCCAAAGTCT  
 ATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCCCAGGGGGTGCAGGATACCCACCTTAA  
 AGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGGTCTCTCGGGACTTCAGACACTGGAAAACCTGGATGC  
 TGCAGACACTGAACGAGGAGCCAGTGACACCAGAGCCGGAAGTGAACCGCCCACTGCCCCCGAGCTCAAGCAAG  
 GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTCACAAAGGCGACCACTTTATCAAGTTCTTCGCTC  
 CGTGGTGTGGTCACTGCAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCTTGAACATTCCGAAACTG  
 TCAAGATTGGCAAGTTGATTGTACACAGCACTATGAACTCTGCTCCGGAACCCAGGTTCTGGCTATCCCACTC  
 TTCTCTGGTTCCGAGATGGGAAAAAGGTGGATCAGTACAAGGGAAAGCGGGATTTGGAGTCACTGAGGGAGTACG  
 TGGAGTCGAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCACGCCCTCAGAGGCCCCGGTGTGGCAG  
 CTGAGCCCCGAGGTGACAAGGGCACTGTGTTGGCACTCACTGAAAATAAATTCGATGACACCATTCAGAAAGGAA  
 TAACCTTCATCAAGTTTATGCTCCATGGTGTGGTCACTGTAAGACTCTGGCTCCTACTTGGGAGGAACTCTCTA  
 AAAAGGAATTCCTGGTCTGGCGGGGGTCAAGATCGCCGAAGTAGACTGCAGTCTGTAACGGAATATCTGCAGCA  
 AGTATTCGGTACGAGGTACCCACGTTATTGCTTTTCCGAGGAGGGAAGAAAGTCAGTGAGCACAGTGGAGGCA  
 GAGACCTTGACTCGTTACACCGCTTTGTCTGAGCCAAAGCGAAAGACGAACCTTAGGAACACAGTTGGAGGTAC  
 CTCTCTGCCCCAGCTCCCGCACCTGCGTTTAGGAGTTCACTCCACAGAGGCCACTGGGTTCCAGTGGTGGCT  
 GTTCAGAAAAGCAGAACATATAAGCGTGAGGTATCTTCTTGTGTGTGTGTTTCCAAGCCACACACTCTACAG  
 ATTCTTTATTAAGTTAAGTTTCTCTAAGTAAATGTGTAACCTCATGGTCACTGTGTAAACATTTTCACTGGCGATA  
 TATCCCCCTTTGACCTTCTCTGATGAAATTTACATGGTTTCTTTGAGACTAAAATAGCGTTGAGGGAAATGAAA  
 TTGCTGGACTATTTGTGGCTCCTGAGTTGAGTGATTTTGGTGAAAGAAAGCACATCCAAAGCATAGTTTACCTGC  
 CCACGAGTTCTGGAAAGGTGGCCCTTGTGGCAGTATTGACGTTCTCTGATCTTAAGGTACAGTTGACTCAATAC  
 TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACCTCTGGAAGATACCTTCACGGCCGCTGC  
 TGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC  
 GTGCCCTGAGTAAGAGAATGCTGATGCCATAACTTTATGTGTGATACTTGTCAAATCAGTTACTGTTCAAGGGGAT  
 CCTTCTGTTTCTCACGGGGTGAAACATGTCTTTAGTTCTCTCATGTTAACACGAAGCCAGAGCCACATGAACTGT  
 TGGATGTCTTCTTAGAAAGGGTAGGCATGGAAAATTCACGAGGCTCATTCTCAGTATCTCATTAACCTCATTTGA  
 AAGATTCAGTTGTATTTGTACCTGCGGTGACAAGACCAGACAGGCTTTCCAGGCCTGGGTATCCAGGGAGGC  
 TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCCTTTTAGAGG  
 CTTGCTATACTTGGTCTGCTTCAAGGAGGTGCACCTTCTAATGTATGAAGAATGGGATGCATTTGATCTCAAGAC  
 CAAAGACAGATGTGAGTGGGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTA  
 ACTCATGCTGTCTTGTGATTAAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCTCTAAGATA  
 GATAGGTGTTTGTCTTTTACCATCGAGCTACTTCCATAATAACCACTTTGCATCCAACACTCTTCACCCACCT  
 CCCATACGCAAGGGGATGTGGATACTTGGCCCCAAAGTAAGTGGTGGTAGGAATCTTAGAAACAAGACCACTTATA  
 CTGTCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACCAGCCTCTGCCTTAAAGGAAATCTTTATTAATCACG  
 TATGGTTCACAGATAATTCTTTTTTTAAAAAAACCCAACTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTACA  
 CAACTTCAGCTTTGCATCACGAGTCTTGTATTCCAAGAAAATCAAAGTGGTACAATTTGTTTGTTTACACTAT  
 GATACTTTCTAAATAAACTCTTTTTTTTTTAA

09973299.101504

## FIGURE 35

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47629, pI: 5.90, NX(S/T): 0

MPARPGRLLPLLARPAALTALLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS  
KHLYTADMFTHGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAH  
SDVCSAQGVRYPTLKLKFKPGQEAVKYQGPRDFQTLNWMQLQTLNEEPVTPEPEVEPPSAPE  
LKQGLYELSASNFEHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT  
QHYELCSGNQVRGYPTLLWFRDGGKVDQYKGRDLESLEYVESQLQRTETGATETVTPSEA  
PVLAAEPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA  
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL

**Signal sequence:**

amino acids 1-32

09078299.101501  
TOTOT"66284660

## FIGURE 36

CTTTTCTGAGGAACCACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT  
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA  
CCGCTGAAGTCTGTGCCACACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA  
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA  
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGA  
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT  
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT  
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT  
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCCG  
GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC  
CAAGAGTGGCTTCTTTCGGGTGTTTATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA  
TGTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC  
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG  
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT  
ACGTATTTGCTATTTTCCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTCCTG  
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT  
CCATCATCAAAAAAAAAAAAAAAAAA

0973299.101501



## FIGURE 37

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDPEEG  
KHGKVGRMGPKGIKGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKKGAGTVCDGCRY  
RKFBVGQLDISIARLKTSMKFVKNVIAGIRETEEFYIYVQEEKNYRESLTHCRIRGGMLAMP  
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC  
VEMLSSGRWNDTECHLTMYFVCEFIKKKK

**Signal peptide:**

amino acids 1-25

09978299.101501  
F05101"66282660

# FIGURE 38

GGTTCTATCGATTTCGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC  
 CCACGCGTCCGCTGCTCTCCGCCCCTGTGGAGTGGTGGGGGCTGGGTGGGAATGGGCGTGT  
 GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT  
 CGGAAGGGAGGATCAGGGATGTTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGC  
 GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA  
 AGCTACACCTCTGGCCGCGAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTGCGGTGCGAGCT  
 CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCGGAAGG  
 TCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACCTGGCCAGCAGCGCGCCGCGC  
 ACACCTTTCTCATTACGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC  
 AGGGCTGCACGCGCCTTCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGGCGACAG  
 CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGGAGCCGGAGATGCAGCGGCCG  
 GAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCCGCCCT  
 CTGTCACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCCAGAGTTTCTGTGGCTCTG  
 GTTCGGGCTGGCCAAGGCCGCGCTGCGCACTGCCTTTGTGCCACCGCCCTGCGCCGGGGCC  
 CCCTGCTGCACTGCCTCCGCGAGCTGCGGCGCGCGCGCGCTGGTGCTGGCGCCAGAGTTTCTG  
 GAGTCCCTGGAGCCGACCTGCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGG  
 CCCAGGAACCCACCCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG  
 GGCCAGTGCCAGGATACTCTCTTCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTC  
 ACCTCTGGCACCACGGGCCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG  
 CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCAC  
 TCTACCACATGTCCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG  
 GTGCTGAAATCCAAGTTCTCGGCTGGTCAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC  
 GGTGTTCCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACCAGCCCCCGAGCAAGGCAG  
 AACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCAGATACTGGGAGCGT  
 TTTGTGCGGCGCTTCGGGCCCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT  
 GGCCACCATCAACTACAGACAGCGGGGCGCTGTGGGGCGTGCTTCCTGGCTTTACAAGC  
 ATATCTTCCCCCTTCTCCTTGATTGCTATGATGTCAACACAGGAGAGCCAATTCCGGACCCC  
 CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGCCCGGTAAGCCA  
 GCAGTCCCCATTCTGGGCTATGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGG  
 ATGTCTTCCGCGCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCA  
 GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC  
 CACAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATG  
 GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC  
 CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCTTATGCCCG  
 GCCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG  
 TTCGGATGGCAAATGAGGGCTTCGACCCCAGCACCTGTCTGACCCACTGTACGTTCTGGAC  
 CAGGCTGTAGGTGCCTACCTGCCCCCTCACAACCTGCCCGGTACAGCGCCCTCCTGGCAGGAAA  
 CCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGGG  
 CCGTTGCAGGTGTACTGGGCTGTGAGGGATCTTTTCTATAACCAGAACTGCGGTCACTATTTT  
 GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTCTGACCTAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC  
 TTGGCCGCCATGGCCCAACTTGTTTATTGCAG

09978299-101501

## **FIGURE 39**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913

><subunit 1 of 1, 730 aa, 1 stop

><MW: 78644, pI: 7.65, NX(S/T): 2

MGVCQRTRAPWKEKSQLERAAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLLPL  
LLLKLHLWPQLRWLPADLAFVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ  
RAAHTFLIHGSRFSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERAAPGAGD  
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLRTAFVPTAL  
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA  
EVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL  
ALPLYHMSGSLLGIVGCMGIGATVVLSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP  
SKAERGHKVR LAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW  
LYKHIFPFLIRYDVTTGEPIRD PQGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPPELAQ GK  
LLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEV  
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTETFK  
QQKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARYSALLAGNLRI

### **Type II transmembrane domain:**

amino acids 45-65

### **Other transmembrane domain:**

amino acids 379-398

**cAMP- and cGMP-dependent protein kinase phosphorylation site**  
starting at amino acid 136

### **CUB domain protein motif**

amino acids 254-261

### **putative AMP-binding domain signature**

amino acids 332-343

### **N-glycosylation sites**

amino acids 37-40 and 483-486

0978299.101501  
105101" 66282660

# FIGURE 40

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA  
 CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTCGCTCTC  
 GCTTGTCCATCTCCCTCCCGGGGAGCCGGCGCGCTCCCACCTTTGCCGCACACTCCGGC  
 GAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGAACCTCGGATTGCAGCTCTGAACCC  
 CCATGGTGGTTTTTTTAAACACTTCTTTTCTTCTCTTCTCGTTTTTGATTGCACCGTTTTCCA  
 TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTTGGCTTGCCATCGT  
 CCATCTGGCTTATAAAAGTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCTCGG  
 CTGGCAGAAGGGGGTGACGCTGGGCAGCGGCGAGGAGCGCGCCGCTGCCTCTGGCGGGCTTT  
 CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTACCGAGCTGGATTTGTATG  
 TTGCACCATGCCTTCTTGATCGGGGCTGTGATTCTTCCCCTCTTGGGGCTGCTGCTCTCCC  
 TCCCCGCCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTACGGTGCC  
 AAGGGATTACGCCTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG  
 TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAAC  
 TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGG  
 CATAAGAAATTTGACGAATTTTCCGAGAGCTCCTGGAGAATGCAGAAAAGTCACTAAATGA  
 TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTCAGAAGTCTTCCAGGACCTCT  
 TCACAGAGCTGAAAAGGTACTACACTGGGGGTAATGTGAATCTGGAGGAAATGCTCAATGAC  
 TTTTGGGCTCGGCTCCTGGAACGGATGTTTCAGCTGATAAACCTCAGTATCACTTCAGTGA  
 AGACTACCTGGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCC  
 GGAACTGAAGATTAGGTTACCCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG  
 TGCTGGGCAGAGAAGTTGCAAACCGAGTTTCCAAGGTGAGCCCAACCCAGGGTGTATCCG  
 TGCCCTCATGAAGATGCTGTACTGCCATACTGCTCGGGGGCTTCCCACTGTGAGGCCCTGCA  
 ACAACTACTGTCTCAACGTCAATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG  
 TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGCCATTCAACAT  
 TGAGTCGGTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA  
 ACAGCATGCAGGTGTCTGCAAAGGTCTTTCAGGGATGTGGTCAGCCCAACCTGTCTCCAGCC  
 CTCAGATCTGCCCCGCTCAGCTCCTGAAAATTTTAATACACGTTTTCAGGCCCTACAATCCTGA  
 GGAAAGACCAACAACCTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA  
 AATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCCTACACTATCTGCAAGGACGAGAGC  
 GTGACAGCGGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT  
 GCCTGAGATCATGAATGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACA  
 TCACTCGGCCTGACACTTTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA  
 CTAAAAAACGCCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG  
 CTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCACGGAGTTTGAGTTTGTACCA  
 CAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCCAGCGTGGC  
 CACTCCCTGCTCTCCTGGTCTCTCACCTGCATTGTCTGGCACTGCAGAGACTGTGCAGATA  
ATCTTGGGTTTTTTGGTCAGATGAAACTGCATTTTAGCTATCTGAATGGCCAACTCACTTCTT  
 TTCTTACACTCTTGACAAATGGACCATGCCACAAAAAATTACCCTTTTCTATGAGAAGAGAG  
 CAGTAATGCAATCTGCCTCCCTTTTTGTTTTTCCCAAAGAGTACCGGGTGCCAGACTGAACTG  
 CTTCTCTTTTCTTTCAGCTATCTGTGGGGACCTTGTATTATTCTAGAGAGAATTCTTACTCAA  
 ATTTTTTCGTACCAGGAGATTTTCTTACCTTCATTTGCTTTTATGCTGCAGAAGTAAAGGAAT  
 CTCACGTTGTGAGGGTTTTTTTTTCTCATTATAAAT

0993299.101501

## FIGURE 41

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADV KARSCEVRQAYGAKGFS LADIPYQEIAGEHLRICPQ  
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMF  
VRTYGMLYMQNSEVFQDLFTELKRYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFSEDY  
LECVSKYTDQLKPFQDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL  
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAERLEGPFNIES  
VMDPIDVKISEAIMNMQENSMQVSAKVFQCGQPKPAPALRSARSAPENFNTRFRPYNPEER  
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHASKARYLPE  
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG  
SGSGCMDDVCPTFEFEFVTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

**Signal peptide:**

amino acids 1-23

09978299.101501  
T05T0T"66282660

## FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAGAAGCTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG  
CAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACCTACGCAAAGACCAAGCGGGCTCCGCGCGGACCGGCCGCGGGC  
TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT  
GGAGGGAGATCAGGAAACGGCTTCTTCTCACTTCGCCGCTGGTGAGTGTGCGGGGAGATTGGCAAACGCCTAGG  
AAAGGACTGGGGAAGATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGTCCACTACGGCAGTTTATCTG  
TCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAGTTCTTTCCAGGTGTGGGGACCGCAGGACAGACGGCCGA  
TCCCCGCCCTCCGTACCAGCACTCCCAGGAGAGTCAGCCTCGCTCCCAACGTGAGGGCGCTCTGGCCACGA  
AAAGTTCCTGTCCACTGTGATTCTCAATTCCTTGCTTGGTTTTTTTCTCCAGAGAACTTTTGGGTGGAGATATTA  
ACTTTTTTCTTTTTTTTTTTCTTGGTGGAAGCTGCTCTAGGGAGGGGGAGGAGGAGGAGAAAGTGAAATGTGC  
TGGAGAAGAGCGAGCCCTCCTTGTTCTTCCGGAGTCCCATCCATTAAGCCATCACTTCTGGAAGATTAAAGTTGT  
CGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTCACCGTCTGTTGGGTGCATG  
TGTGCGCCCGCAGCGGCGCGGGGCGCGTGGTTCTCCGCGTGGAGTCTCACCTGGGACCTGAGTGAATGGCTCCCA  
GGGGCTGTGCGGGGCATCCGCCTCCGCCTTCTCCACAGGCCTGTGTCTGTCTGGAAGATGCTAGCAATGGGGG  
CGCTGGCAGGATTCTGGATCCTCTGCCTCCTCACTTATGGTTACCTGTCTGGGGCCAGGCCTTAGAAGAGGAGG  
AAGAAGGGGCCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCACAACCTCCACCTCCCAGCCCCATCTCA  
TTTTCATCCTAGCGGATGATCAGGGATTTAGAGATGTGGGTACCACGGATCTGAGATTAAACACCTACTCTTG  
ACAAGCTCGCTGCCGAAGGAGTTAAACTGGAGAACTACTATGTCCAGCCTATTTGCACACCATCCAGGAGTCAGT  
TTATTACTGGAAGTATCAGATACACACCGGACTTCAACATTCTATCATAAGACCTACCCAACCAACTGTTTAC  
CTCTGGACAATGCCACCCTACCTCAGAACTGAAGGAGGTTGGATATTCAACGCATATGGTCGGAAAATGGCACT  
TGGGTTTTTAACAGAAAAGATGCATGCCACCAGAAGAGGATTTGATACCTTTTTTGGTTCCCTTTTGGGAAGTG  
GGGATTACTATACACTACAAATGTGACAGTCTTGGGATGTGTGGCTATGACTTGTATGAAAACGACAATGCTG  
CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCATA  
ACCCACAAAGCCTATATTTTATATACTGCCTATCAAGCTGTTTATTACCACTGCAAGCTCCTGGCAGGTATT  
TCGAACACTACCGATCCATTATCAACATAACAGGAGAAGATATGCTGCCATGCTTTCTGCTTAGATGAAGCAA  
TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAACAACAGCATTATCATTTACTCTTCAGATAATG  
GTGGCCAGCCTACGGCAGGAGGGAGTAACTGGCCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC  
GGGCTGTAGGCTTTGTGCATAGCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACCTGTGCACATCACTG  
ACTGGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT  
GGGAGACCATAAGTGAGGGTCTTCGCTCACCCCGAGTAGATATTTTGATAACATTGACCCCTATACACCAAGGC  
AAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG  
GAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTCAGCAACCTGGGACCGAACCG  
GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGA  
GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAAC  
TGCAGTGCCGGTCAGGTATCCCCCAAGACCCAGAAAGTAACCTAGGCTCAATGGAGGGGTCTGGGGACCATG  
GTATAAAGAGGAAACCAAGAAAAAGCAAGCAAAAATCAGGCTGAGAAAAAGCAAAAGAAAAGCAAAAAAA  
GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACAGCAAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA  
GGCTTGTTTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCACACTGAAAAGTGTCTGCTCAGTG  
CCAAGGTGCTACTCTTGCAAGCCACACTTAGAGAGAGTGGAGATGTTTATTTCTCTCGCTCCTTTAGAAAACGTG  
GTGAGTCTTGAGTTCCACTGCTGTGCTTCAGTCAACTGACCAAACTGCTTTGAATTATAGGAGGAGAACATA  
ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAACTACCTTTGATAAATTAC

09978299.101501

## FIGURE 42B

AGTCAAAGATTGTGTCACCTCAAAGGCCTTGAAGAATATATTTTCTTGGTGAATTTTGTATGTCTGTGCATATGA  
CACTTGGGTTTTTTAATTAATTCTATTTTATATATATAAATATATGTTTCTTTTCTGTGAAAAGCTGTTTTTCT  
CACATGTGAACAGCTTGCACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCCC  
ACAATGAATGTAACATTTTTCTAAACACTTTACTAGAAGAACATTTTCACTATAAAAAACCTAATTTATTTTACA  
GAAAAATATTTTGTGTTTTTATAAAAAGTTATGCAAATGACTTTTATTTTATTTTCTGTGCATACCATTAGAAGA  
ATTTTATTTTCACTTCTTCAAATTATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTCAGACTA  
TAAAAACATCATTAGAAAACCTTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT  
ATTACTTGGAATTCATGTTTGTGTCAGAGTTGAGACAACTTTATTGTTTCTATCATAAACTATTTATGTATCTT  
AATTATTAAAATGATTTACTTTATGGCACTAGAAAATTTACTGTGGCTTTTCTGATCTAACTTCTAGCTAAAATT  
GTATCATTGGTCCTAAAAATAAAAATCTTTACTAATAGGCAATTGAAGGAATGGTTTGCTAACAACCACAGTAA  
TATAATATGATTTTACAGATAGATGCTTCCCCTTGGCTATGACATGGAGAAAGATTTTCCCATAATAATACTAA  
TATTTATATTAGGTTGGTGCAAACTAGTTGCGGTTTTTCCCATTAAGTAATAACCTTACTCTTATACAAAGT  
GGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCCTGGAGTAGGTAACCTTGCTTGAAACCCC  
ACATGCAAACGTCATGAGGAGAATTAAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTCATCAATGAGCATA  
GATTGGTGTGGATCCTGTAGACCCTGGTGTTTTCTTTGAAGTGCCCTCTCCTAATGCAGAGGCCTTGAAGCTTAC  
AGTATACACTTGAAAAGTCACAGATAGCTAGAATTATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGT  
GGTGGTATGACAGCATACCATTAAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTTATATCAC  
AACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAATGTATAAAAGAATCTATAAT  
CTAGTACTGAAATTACTAAATTGGGTAAGATGATTTAAATGATTTTAAATTTTAAACATTTTATTTCTAGAATATAT  
GGCTCCATTTTATTTTATAGTGTAAGTTGTATTTCTAAAGTTTGTGTTTTGTGCGACAGTATCTTTTAAATGAG  
TCTTAAAAATAAAGGCATATTGTTTCATGTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

09978299 101501

Figure 1 consists of 11 bar charts (a-k) showing the percentage of total catch for various fish species in the Chesapeake Bay. The species are: a) Atlantic croaker, b) Striped bass, c) Weakfish, d) Spot, e) Blue crab, f) Rockfish, g) Atlantic silverside, h) Atlantic herring, i) Atlantic menhaden, j) Atlantic bluefish, and k) Atlantic tomcod. Each chart compares the percentage of total catch in 1990 (white bars) and 1991 (black bars) across four size classes: 0-10 cm, 10-20 cm, 20-30 cm, and 30-40 cm. The y-axis for all charts is 'Percentage of total catch' ranging from 0 to 100. The x-axis for all charts is 'Size class (cm)'.

><MW: 56885, pI: 6.49, NX(S/T): 5

amino acids 1-37

amino acids 120-132

amino acids 168-177

amino acids 163-169

amino acids 157-160, 306-309 and 318-321



# FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC  
 TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC  
 CCGTGCGAGAATGCCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTGCTCTCCTGGGTGGCAG  
 GTGGTTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTTGTTAGCATCGGCACGTCAGCCT  
 GGGGTCTGTCACTATGGAATAAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG  
 AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAGTGCGTGGGACCAAACAAAT  
 GCAGATGCTTTCCAGGATACACCGGGAAAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG  
 AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTTTTGCCT  
 CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACTCTAGGACATGTGCCATGATAA  
 ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA  
 CTCCGCCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT  
 CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAAATGTCA  
 TTGGTTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT  
 ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCCTTCAAGTG  
 TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTCTGCTATCCCTGAAAATTCTG  
 TGAAGGAAGTCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC  
 AAAACAGCATGAAAAAGAAGGCAAAAATTAATAATGTTACCCAGAACCCACCAGGACTCC  
 TACCCCTAAGGTGAACCTTGACGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGA  
 CTCATGGAGGTAAAAAAGGGAATGAAGAGAAAATGAAGAGGGGCTTGAGGATGAGAAAAGAG  
 AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTTCCCT  
 AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAA  
 ACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT  
 GGAAACAGGATAGAGAAGATGATTTTGAAGTGAATCCTGCTGATCGAGATAATGCTATTGGC  
 TTCTATATGGCAGTTCCGGCCTTGGCAGGTCAAGAAAGACATTGGCCGATTGAACTTCT  
 CCTACCTGACCTGCAACCCCAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG  
 ACAAGTCCGGAAACTTCGAGTGTTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG  
 ACCACGAGTGAGGATGAAAAGTGGAAGACAGGAAAAATTGAGTTGTATCAAGGAAGTATGC  
 TACCAAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGCAAACCGGCGAAATCGCAGTGG  
 ATGGCGTCTTGCTTGTTTTAGGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG  
 TTACTATCTTTATATTTGACTTTGTATGTGAGTTCCCTGGTTTTTTTGTATATTGCATCATAG  
 GACCTCTGGCATTTTGAATTACTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATTG  
 TAAGATGCCTTTCTTGTATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT  
 TCTCAGTCATTTCTGAATCTTTCCNCATTATATTATAAAATNTGGAAANGTCAGTTTATCTC  
 CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA  
 GAAAATAGAAAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGGA  
 AACTATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC  
 TTGTATATTTAATTCTTTGTAATAATAA

09978299-101501

## FIGURE 45

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRNNSKGVCE  
ATCEPGCKFGECVGPKNCRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGSKCFCLSGH  
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP  
YNRRCVNTFGSYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK  
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPPK  
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

### **Signal peptide:**

amino acids 1-21

### **EGF-like domain cysteine pattern signature.**

amino acids 80-91

### **Calcium-binding EGF-like domains**

amino acids 103-124, 230-251 and 185-206

097829 101501  
FOSTOT 6628/660

## FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGCTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG  
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCC  
AGAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGAATTGGTGAGG  
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGCTGTCTAGCCAGAAGAGTGCAT  
GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT  
TGTTTTGCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC  
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAATGTCCCAGCGTTCTCTGTGC  
ATGGATACCAGCTTGGAATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTCT  
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA  
ATAGCATCCTGGGTATCATATCTGTACCTCTTCCATTGGATACTGTGCTAGCAAGCATGCT  
CTCCGGGGTTTTTTTAAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC  
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA  
CAAAGACTATAGGCAATAATGGAGACCAGTCCCACAAGATGACAACCAGTCGTTGTGTGCGG  
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT  
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG  
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAAATC  
TTTAAGACAAAACATTGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG  
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT  
ACTTTTTAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAATAAAG  
ATTGCCATGAATCTTGCAAAA

097899-101501  
F05F01" 66284560

## **FIGURE 47**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343

><subunit 1 of 1, 289 aa, 1 stop

><MW: 32268, pI: 9.21, NX(S/T): 0

MVVWVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPDL  
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQRSCLMDTSLDVYRKLIELNYLGTVSLTKCVL  
PHMIERKQGKIIVTVNSILGIIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIIVSNICPGP  
VQSNIVENSLAGEVTKTIGNNGDQSHKMTTSCVRLMLISMANDLKEVWISEQPFLLVTYLW  
QYMPWAWWITNKMGGKRIENFKSGVDADSSYFKIFKTKHD

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 136-157

#### **Tyrosine kinase phosphorylation site.**

106-113 and 107-114

#### **Homologous region to Short-chain alcohol dehydrogenase**

amino acids 80-90, 131-168, 1-13 and 176-185

09978299-101501  
TOSTOT" 65384560

# FIGURE 48

GCGACGTGGGCACCGCCATCAGCTGTTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC  
 GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTCGG  
 TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCTCTGTCC  
 TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTT  
 TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT  
 GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA  
 ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCTGTG  
 GACAGCGTGGCCCCGGCCCCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC  
 TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC  
 CTGGGTCTCTACTGCTGCCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGGT  
 CAGTGGTCTTGGGTTCTCTGCAGCGTGAAGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG  
 GCTGCCCTGCAGTTGCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT  
 GCAGCTCGCCACCCACGACCCACACACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCC  
 CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC  
 CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGTATCTACAACAGCT  
 GCACCAGCGACACCTGTCCAACCCGGCCCGGCTGGGATGCTATGTGGGGGGCCCCCAGCCTG  
 GGGTGCAGGGCCCCCTGTGAGGAGATTCCGGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGA  
 CACTGGGTTTCAAGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT  
 GCTGCTGACCAACACAGCTGCTCACAGTTCTTGGCTGCAGGCTCGAGTTTCAAGGGGCAGCTT  
 TCCTGGCCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA  
 TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCT  
 GATGCACACAGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTG  
 CTGCCCTGCTTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGA  
 CCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCCTGAGGGGGG  
 CTACGACATGGCCCTCCTGCTGCTGGCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC  
 TCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG  
 GCCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAG  
 GGCTGTCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG  
 TGTGTACCAAGTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCACCAGTGGT  
 CATGAGGTGAGGGGCACATGGTTTCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG  
 CCCCCGCCAGGCCGGCGGTCTTACCGCGCTCCCTGCCCTATGAGGACTGGGTGAGCAGTTTGG  
 ACTGGCAGGTCTACTTCGCCGAGGAACAGAGCCCGAGGCTGAGCCTGGAAGCTGCCTGGCC  
 AACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC  
 AGGCAGGCAAATGGCATTACTGCCCCTGTCTCCCCACCCTGTCATGTGTGATTCCAGGCAC  
 CAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCCA  
 CTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCACACCCAACTCTGCTACCAAGC  
 AGGCGTCTCAGCTTTCCTCCTCCTTTACTCTTTCAGATACAATCACGCCAGCCACGTTGTTT  
 TGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCTTTTTTTAACTTAAATAAATTGTTAC  
 AAAATAAAA

0976299.101501

## **FIGURE 49**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV  
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA  
EEVGVAALQLPRAYNHYSQGSDDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTS  
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLC  
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDS  
CVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV  
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERG  
WVLGRARPGAGISSLQTVPVTLTGPRACSRLLHAAPGGDGSPILPGMVCTSAVGELPSCEGLS  
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAE  
GSCLANISQPTSC

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **Homologous region to Serine proteases, trypsin family**

amino acids 79-95, 343-359 and 237-247

#### **N-glycosylation sites.**

amino acids 37-40 and 564-567

#### **Kringle domains**

amino acids 79-96, 343-360 and 235-247

09978299.101501  
"66282660"

# FIGURE 50

CGGGCCGCCCCCGGCCCCCATTCGGGCGGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG  
 GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGGCGCGGCAGGGGCAGCCTTCCACCACGGGGAG  
 CCCAGCTGTCAGCCGCCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGT  
 GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG  
 TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCC  
 CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATAACCAAACA  
 GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC  
 TCTTCCCGGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGGTGCGTGTGGCG  
 GACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCCGGCAGCGCTGCCGTACGCTT  
 GCAGGTGGCCGCTCCCTACTCGAAGCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC  
 CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTT  
 TGGCAGGATGGGCAGGGTGTGCCCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAACGA  
 GCAGGGCTTGTTTGATGTGCACAGCGTCCTGCGGGTGGTGTGCGGTGCGAATGGCACCTACA  
 GCTGCCTGGTGCACAAACCCGCTGCTGCAGCAGGATGCGCACRGCTCTGTACCATCACAGGG  
 CAGCCTATGACATTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT  
 TGCAGTGTGCTGGTGGCCCTGGCTTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAG  
 AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT  
 CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGG  
 GAGCTGCTACCCCTCCCTACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC  
 TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCAAAGGATGCGATACAC  
 AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTT  
 TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT  
 GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCTC  
 TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTGAGA  
 CTGACTGACCCCTGCCTTATTTACCAAAGACACGATGCATAGTCACCCCGGCCTTGTTTC  
 TCCAATGGCCGTGATACACTAGTGATCATGTTTCAGCCCTGCTTCCACCTGCATAGAATCTTT  
 TCTTCTCAGACAGGGACAGTGCGGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCTTTT  
 CCCTCCTTCCCTCCCTGCCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG  
 AGGGGACTGCCCCCACCACCATGGTGTCTATTCTGGGGCTGGGGCAGTCTTTTCTGGC  
 TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG  
 GATGTCATCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC  
 TCGGAGGGATTTGTAAACTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAAAA  
 AAAAAAAAAAAAAA

097829.101501

## FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386

><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQ  
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFV  
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDVTITCSSYQGYPEAEVFWQDGQGVPL  
TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA  
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGELEGSKTALQPLKHSDSKED  
DGQEIA

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 251-270

#### **N-glycosylation site.**

amino acids 91-94, 104-107, 189-192 and 215-218

#### **Homologous region to Immunoglobulins and MHC**

amino acids 217-234

09078299-101501  
TOSTOT" 55284660



## FIGURE 52

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC  
 CTGAACTTGTCTGAAGCCCTTGTCCGTAAGCCTTGAAGTACGTTCTTAAATCTATGAAGTCG  
 AGGGACCTTTTCGCTGCTTTTGTAGGGACTTCTTTTCCTTGCTTCAGCAACATGAGGCTTTTCT  
 TGTGGAACGCGGTCTTGACTCTGTTTCGTCACTTCTTTGATTGGGGCTTTGATCCCTGAACCA  
 GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTTCATCTGCCATCGCAAGACCAAGGAGGGGA  
 TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC  
 ACAAACATAACAATGGTCAGCCCATTGTGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT  
 TGGGACCAGGGCTTGAAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCTCTCTGC  
 TCTGGGCTATGGAAGAAGGAAAAGGTAAAATTCCTCCAGAAAGTACACTGATATTTAATA  
 TTGATCTCTGGAGATTCGAAATGGACCAAGATCCCATGAATCATTCGAAGAAATGGATCTT  
 AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGA  
 ACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTGGATAAAG  
 AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA  
TAGAGATACATCTACCCTTTTAAATATAGCACTCATCTTCAAGAGAGGGCAGTCATCTTTAA  
 AGAACATTTTATTTTATACAATGTTCTTTCTTGCTTTGTTTTTATTTTATATATTTTTT  
 CTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT  
 GGGAAAGAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTCACTTTCACAG  
 ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACC  
 ACGACATGAGACCAGGTTATAGCACAAATTAGCACCCCTATATTTCTGCTTCCCTCTATTTTC  
 TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT  
 GTTATAATGAAATAGTTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA  
 TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG  
 TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAG  
 GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA  
 CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCCTGTAATCCCAGCT  
 ACCCAGGAAGGCTGAGGCGGCAGAACTCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAG  
 ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAGAAAAGAACACGGTTAATACCATATNA  
 ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGAT  
 TGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG  
 TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC  
 TAGCGGAATATCCTTCCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA  
 TTGTATCATAAGATAAAGTAGTAAACCAGTCTACATTTTCCATTTCTGTCTCATCAAAAAC  
 TGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGGGCCAAGGAGGG  
 TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTA  
 CTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGACACCTGTAGTCCCAGCTACTCGGGAG  
 GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC  
 ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAGAAGCAGA  
 CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

09078299-101501

## FIGURE 53

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194

><subunit 1 of 1, 211 aa, 1 stop

><MW: 24172, pI: 5.99, NX(S/T): 1

MRLFLWNAVLTLFVTSLLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSL  
FHSTHKHNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPEST  
LIFNIDLLLEIRNGPRSHESFQEMDLNDDWKLKDEVKAYLKKEFEKHGAVVNESHHDALVED  
IFDKEDDKDGFISAREFTYKHDEL

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **N-glycosylation site.**

amino acids 176-179

#### **Casein kinase II phosphorylation site.**

amino acids 143-146, 156-159, 178-181 and 200-203

#### **Endoplasmic reticulum targeting sequence.**

amino acids 208-211

#### **FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 78-114 and 118-131

#### **EF-hand calcium-binding domain.**

amino acids 191-203, 184-203 and 140-159

#### **S-100/ICaBP type calcium binding domain**

amino acids 183-203

09978299-101504

# FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCAT  
 CCAACCATTCCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCCCTCTCCCGTAGCCCCACCCGA  
 CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT  
 CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTAC  
 CTGCCACCCTCAACGTCTCAATGGCTCTGACGCCCGCCTGCCCTGCACCTTCAACTCCTGC  
 TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTC  
 TGAGGAGATGTTCCCTCCAGTTCGCGATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAG  
 ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGCGGTGATGCTGAGAAACGTG  
 CAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCCTGACCGCCACCGTGG  
 CCATGGCAAGATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG  
 CCGTGATTGTGGGTGCCTCCGTGCGGGGCTTCTGGCTGTGGTTCATCTTGGTGCTGATGGTG  
 GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA  
 GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCC  
 CTGCAGCCTCCCGTGTCCCGTCTCCTCCCTCTCCGCCCTGTACAGTGACCTGCCTGCTCG  
 CTCTTGGTGTGCTTCCCGTGACCTAGGACCCAGGGCCACCTGGGGCCTCCTGAACCCCCG  
 ACTTCGTATCTCCACCCCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA  
 TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCACCTGCCAGTCCCTGG  
 GGGGAGGCAGGAGGCACATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA  
 GGAGGGGCCGCTGTACCTGCCAGTGCTTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGG  
 GGAGGGAGGGCTTCTCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTG  
 TGCTCCTCCCTGCTCCCAGCCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGA  
 AACTTGAGGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGG  
 CTGCAGGCAAAGCTGGACATGTGCCCTGGCCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT  
 GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG  
 ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCAGCGGGGACCCACCAACAGAGGCC  
 AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTGTGCTGCAG  
 GCTCTGCCTTCTCCATGGGGTAACCAACCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT  
 GAGGAGGCCATGCACAGGGTGGGGCAGCTTTCTTTGGGGCTTCAGTGAGAACTCTCCAGTT  
 GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAGGGAAAGCCTGAGGCCG  
 GCATAAGGGGAGGCCTTGAACCTGAGCTGCCAATGCCAGCCCTGTCCCATCTGCGGCCACG  
 CTACTCGCTCCTCTCCCAACAACCTCCCTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC  
 ACAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGGATTACCTCCAT  
 CTGTTTGTAGTAAATGGGCAAAACCCCATCTCTACTAAAAATACAAGAATTAGCTGGGCGTG  
 GTGGCGTGTGCCTGTAATCCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG  
 GGAAGCAGAGGTTGCAGTGAACCTGAGATAGTGATAGTGCCACTGCAATTCAGCCTGGGTGAC  
 ATAGAGAGACTCCATCTCAAAAAA

0978299-101504

## FIGURE 55

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNNGSDARLPCTFNSCYTVNHKQ  
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRVQPEDEGI  
YNCYIMNPPDRHRGHGKIHLLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRK  
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 161-179

#### **Immunoglobulin-like fold:**

amino acids 83-127

#### **N-glycosylation sites.**

amino acids 42-45, 66-69 and 74-77

09978299-101E01  
F05T0T"6282660

## FIGURE 56

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTTAGCATCCAACCATCCTCCCTTGTA  
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA  
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT  
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC  
TCAATGGCTCTGACGCCCCGCCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC  
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCCCTCCAG  
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG  
GAACCCCAGCAAGTACGATGTGTGCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA  
TTTACAACCTGCTACATCATGAACCCCCC

09978299-101501  
T05T0T 66282660

## FIGURE 57

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCCACCAGGACGGAGCATGGAGGTNCACATA  
CCTGCCACCCTCAACGTCCTCAATGGCTTTGACGCCCCGCCTGCCCTGCACCTTCAACTCCNG  
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACCTGGC  
TCTGAGGAGATGTTCCCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG  
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCAGCAAGTACGATGTGTCGGTGATGC  
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCC

09978299 " 101501  
105101 66282660

# FIGURE 58

TGCGGCGACCGTCTGTACACCAATGGGCCTCCACCTCCGCCCCCTACCGTGTGGGGCTGCTCCCGGATGGCCTCCTGT  
TCCTCTTGCTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCCGGCCGACGTCAACCCAGTGGTGTGGTCC  
CTGGTGATTTGGGTAACCAACTGGAAGCCAAGCTGGACAAGCCGACAGTGGTGCACTACCTCTGCTCCAAGAAGA  
CCGAAAGCTACTTCACAATCTGGCTGAACCTGGAAGTGTGCTGCCTGTCACTATTGACTGCTGGATTGACAATA  
TCAGGCTGGTTTACAACAAAACATCCAGGGCCACCCAGTTTCTTGATGGTGTGGATGTACGTGTCCCTGGCTTTG  
GGAAGACCTTCTCACTGGAGTTCTTGGACCCAGCAAAAGCAGCGTGGGTTCCTATTTCCACACCATGGTGGAGA  
GCCTTGTGGGCTGGGGCTACACACGGGGTGAGGATGTCCGAGGGGCTCCCTATGACTGGCGCCGAGCCCCAAATG  
AAAACGGGCCCCTACTTCCCTGGCCCTCCGCGAGATGATCGAGGAGATGTACCAGCTGTATGGGGGCCCGTGGTGC  
TGGTTGCCCCACAGTATGGGCAACATGTACACGCTCTACTTTCTGCAGCGGCAGCCGAGGCCCTGGAAGGACAAGT  
ATATCCGGGCCCTTCTGTCTCACTGGGTGCGCCCTGGGGGGGCGTGGCCAAGACCCCTGCGCGTCTTGGCTTCAGGAG  
ACAACAACCGGATCCCAGTCACTCGGGCCCCCTGAAGATCCGGGAGCAGCAGCGGTGAGCTGTCTCCACCAGCTGGC  
TGCTGCCCTACAACTACACATGGTCACCTGAGAAGGTGTTCTGTGCAGACACCCACAATCAACTACACACTGCGGG  
ACTACCGCAAGTTCTTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGG  
AAGCCACGATGCCACCTGGCGTGCAGCTGCACTGCCTCTATGGTACTGGCGTCCCCACACCAGACTCCTTCTACT  
ATGAGAGCTTCCCTGACCGTGACCCCTAAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACCTGAAGAGTGCCC  
TGCAGTGCCAGGCCTGGCAGAGCCGCCAGGAGCACCAAGTGTGCTGCAGGAGCTGCCAGGCAGCGAGCACATCG  
AGATGCTGGCCAAACGCCACCACCCCTGGCCTATCTGAAACGTGTGCTCCTTGGGCCCCTGACTCCTGTGCCACAGGA  
CTCCTGTGGCTCGGCCGTGGACCTGCTGTTGGCCTCTGGGGCTGTGATGGCCCACGCGTTTTTGCAAAGTTTGTGA  
CTCACCATTCAAGGCCCCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGTGTTTGTATCCTTTCTCT  
GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAATGCTGCTGATGGTGGGA  
ACTGCTGTGACCTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGGCCCTGGTCCCAGTCCCTGCCCTGGGGCCATG  
TGTCCCCCTATTCTGTGGGCTTTTCATACCTTGCCCTACTGGGCCCTGGCCCCGAGCCTTCCCTATGAGGGATGTT  
ACTGGGCTGTGGTCTGTACCCAGAGGTCCCAGGGATCGGCTCCTGGCCCCCTCGGGTGACCTTCCCACACACCA  
GCCACAGATAGGCCTGCCACTGGTCACTGGGTAGCTAGAGCTGCTGGCTTCCCTGTGGCTTAGCTGGTGGCCAGCC  
TGACTGGCTTCCCTGGGCGAGCCTAGTAGCTCCTGCAGGCAGGGGCAGTTTGTGCGTTCTTCGTGGTTCCCAGGC  
CCTGGGACATCTCACTCCACTCCTACCTCCCTTACCACCAGGAGCATTCAAGCTCTGGATTGGGCAGCAGATGTG  
CCCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCTGATTTCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGC  
CTCCCTTACCCCTGGGACTGTGGTTCCAAGGATGAGAGCAGGGGTTGGAGCCATGGCCTTCTGGGAACCTATGGA  
GAAAGGGAATCCAAGGAAGCAGCCAAGGCTGCTCGCAGCTTCCCTGAGCTGCACCTCTTGCTAACCCACCATCA  
CACTGCCACCCCTGCCCTAGGGTCTCACTAGTACCAAGTGGGTGAGCACAGGGCTGAGGATGGGGCTCCTATCCAC  
CCTGGCCAGCACCCAGCTTAGTGCTGGGACTAGCCCAGAACTTGAATGGGACCCTGAGAGAGCCAGGGGTCCCC  
TGAGGCCCCCTAGGGGCTTTCTGTCTGCCCCAGGGTGTCCATGGATCTCCTGTGGCAGCAGGCATGGAGAGT  
CAGGGGTGCCCTCATGGCAGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCGAGAAAAGGTTACAGCCTCTAGGT  
GGGGTTCCCAAAGACGCCCTCAGGCTGGACTGAGCTGCTCTCCACAGGGTTTCTGTGCAGCTGGATTTTCTCTG  
TTGCATACATGCCTGGCATCTGTCTCCCTTGTTCCTGAGTGGCCCCACATGGGGCTCTGAGCAGGCTGTATCTG  
GATTCTGGCAATAAAAGTACTCTGGATGCTGTAAAAA

## **FIGURE 59**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189

><subunit 1 of 1, 412 aa, 1 stop

><MW: 46658, pI: 6.65, NX(S/T): 4

MGLHLRPYRVGLLPDGLLFLLLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH  
YLCSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDRVPGFGKTFSL  
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEMYQ  
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI  
PVIGPLKIREQQRSAVSTSWLLPYNYTWSPEKVVFVQTPTINYTLRDYRKFFQDIGFEDGWL  
MQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ  
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLG

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Potential lipid substrate binding site:**

amino acids 147-164

#### **N-glycosylation sites.**

amino acids 99-102, 273-276, 289-292 and 398-401

#### **Lipases, serine proteins**

amino acids 189-201

#### **Beta-transducin family Trp-Asp repeat**

amino acids 353-365

097829-101501  
TOSTOT" 55284660



## FIGURE 60

CGGACGCGTGGGCGGACGCGTGCGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGG  
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA  
GGTGGTGGCGCGCGCCGTGTGCTTGCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTG  
AGGGCTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT  
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGT  
GGTCGACGCGTATTTCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG  
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTTGTTGGTTTTCTGCTTCCTCACCAAC  
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCGGACTCTGTGAGGGCAGCCAT  
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT  
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT  
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAA  
CGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTTGAGTGGCGGTTAGCGTGGGAA  
GGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAAGTGCCA  
GCCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC  
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCT  
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTAGCTAGTGTTTTTCTCGCTTTTAATGA  
CCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT  
CAGCTTCCCCCGGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG  
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCA  
CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT  
GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTG  
CTCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCAGCTTTATGTAAATATTC  
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTC  
TGTGCCGAGTGATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACG  
GAATAAATGTTTTCTCATTCAAAG

09078299-101501

## FIGURE 61

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEYSNAHESKQMYCVFN  
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFWLVGFC  
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP  
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

### **Important features:**

#### **Type II Transmembrane domain:**

amino acids 1-45

#### **Other transmembrane domains:**

amino acids 74-90, 108-126 and 145-161

#### **N-glycosylation site.**

amino acids 97-100

09078299-101501  
TOSTOT"6282660

# FIGURE 62

GAGCCACCTACCCTGCTCCGAGGCCAGGCCTGCAGGGCCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG  
 CCCGTGGCCGAGGCCCCCAGGTGGCTGGCGGGCAGGGGACGGAGGTGATGGCGAGGAAGCGGAGCCAGAGGGG  
 ATGTTCAAGGCCTGTGAGGACTCCAAGAGAAAAGCCCCGGGGCTACCTCCGCCTGGTGCCCTGTTTGTGCTGCTG  
 GCCCTGCTCGTGCTGGCTTCGGCGGGGGTGTACTCTGGTATTTCTAGGGTACAAGGCGGAGGTGATGGTCAGC  
 CAGGTGTACTCAGGCAGTCTGCGTGTAATCGCCACTTCTCCAGGATCTTACCCGCCGGGAATCTAGTGCC  
 TTCCGCAGTGAAACCGCCAAAGCCCAGAAGATGCTCAAGGAGCTCATCACCAGCACCCGCTGGGAACCTTACTAC  
 AACTCCAGCTCCGTCTATTCTTTGGGGAGGGACCCCTCACCTGCTTCTTCTGGTTTATTCTCCAAATCCCCGAG  
 CACCGCCGGCTGATGCTGAGCCCCGAGGTGGTGCAGGCACTGCTGGTGAGGAGCTGCTGTCCACAGTCAACAGC  
 TCGGCTGCGCTCCCTTACAGGGCCGAGTACGAAGTGGACCCCGAGGGCCTAGTGATCCTGGAAGCCAGTGTGAAA  
 GACATAGCTGCATTGAATTCACGCTGGGTGTGTTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCCTCCGGCTG  
 AAGGGGCTGACCACCTGGCCTCCAGCTGCCTGTGGCACCTGCAGGGCCCCAAGGACCTCATGCTCAAACCTCCGG  
 CTGGAGTGACGCTGGCAGAGTGCCGGGACCGACTGGCCATGTATGACGTGGCCGGGCCCCCTGGAGAAGAGGGCTC  
 ATCACCCTCGGTGTACGGCTGCAGCCGCCAGGAGCCCGTGGTGGAGGTTCTGGCGTCGGGGGCCATCATGGCGGTG  
 GTCTGGAAGAAGGGCCTGCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCCAGGCCTGT  
 GAAGTGAACTGACGCTGGACAACAGGCTCGACTCCAGGGCGTCTCAGCACCCCGTACTTCCCCAGCTACTAC  
 TCGCCCCAAACCACTGCTCCTGGCACCTCACGGTGCCCTCTCTGGACTACGGCTTGGCCCTCTGGTTTGTATGCC  
 TATGCACTGAGGAGGCAGAAGTATGATTTGCCGTGCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGT  
 GGCTTGCGCATCCTGCAGCCCTACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTACC  
 TCCAGATCTCCCTCACCGGGCCCCGGTGTGCGGGTGCAGTATGGCTTGTACAACAGTCCGACCCCTGCCCTGGA  
 GAGTTCCCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCTGTGATGGGGTCAAGGACTGCCCAACGGCCTGGAT  
 GAGAGAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGACAGCACATGCATCTCACTGCCCCAAGGTCTGT  
 GATGGGCAGCCTGATTGTCTCAACGGCAGCGATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACC  
 TTCCAGTGTGAGGACCGGAGCTGCGTGAAGAAGCCCAACCCGAGTGTGATGGGCGGCCGACTGCAGGGACGGC  
 TCGGATGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGATTGTTGGTGGAGCTGTGTCCTCCGAG  
 GGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCCGGGGTGCACACATCTGTGGGGGGGCCCTCATCGCTGACCGC  
 TGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCATGGCCTCCACGGTGTGTGGACCGTGTTCCTGGGC  
 AAGGTGTGGCAGAACTCGCGCTGGCCTGGAGAGGTGTCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACCAC  
 GAAGAGGACAGCCATGACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCCTCGGCCGCCGTGCGC  
 CCCGTCTGCGCTGCCCGCGCGCTCCCACTTCTTCGAGCCCCGGCCTGCAGTGTGGATTACGGGCTGGGGCGCCTTG  
 CGCAGGGCGGCCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTGATCCACAGGACCTGTGCAGCGAG  
 GCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGCCGCTACCGCAAGGGCAAGAAGGATGCCTGTCAAGGT  
 GACTCAGGTGGTCCGCTGGTGTGCAAGGCACTCAGTGGCCGCTGGTTCTTGGCGGGGCTGGTCAGCTGGGGCCTG  
 GGCTGTGGCCGGCCTAACTACTTCCGGCGTCTACACCCGCATCAGAGTGTGATCAGCTGGATCCAGCAAGTGGTG  
 ACCTGAAGGAATGCCCCCTGCAAAGCAGGGCCACCTCCTGGACTCAGAGAGCCAGGGCAACTGCCAAGCAGG  
 GGGACAAGTATTCTGGCGGGGGGTGGGGGAGAGAGCAGGCCCTGTGGTGGCAGGAGGTGGCATCTTGTCTCGTCC  
 CTGATGTCTGCTCCAGTGATGGCAGGAGGATGGAGAAGTGCCAGCAGCTGGGGGTCAAGACGTCCCTGAGGACC  
 CAGGCCACACCCAGCCCTTCTGCTCCCAATTCTCTCTCTCCTCCGTCCCCTTCTCCACTGCTGCCTAATGCAAG  
 GCAGTGGCTCAGCAGCAAGAATGCTGGTTCTACATCCGAGGAGTGTCTGAGGTGCGCCCCACTCTGTACAGAGG  
 CTGTTTGGGCAGCCTTGCTCCAGAGAGCAGATTCCAGCTTCGGAAGCCCCCTGGTCTAATTGGGATCTGGGAAT  
 GGAAGGTGCTCCCATCGGAGGGGACCCCTCAGAGCCCTGGAGACTGCCAGGTGGGCCTGCTGCCACTGTAAAGCCAA  
 AAGGTGGGAAGTCTGACTCCAGGGTCTTGGCCCCACCCCTGCCTGCCACCTGGGGCCTCACAGCCCAGACCCCT  
 CACTGGGAGGTGAGCTCAGCTGCCCTTTGGAATAAAGCTGCCTGATCAAAAAAAAAAAAAAAAAAAAAA

09973299.101501

## FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152

><subunit 1 of 1, 802 aa, 1 stop

><MW: 88846, pI: 6.41, NX(S/T): 7

MPVAEAPQVAGGQGDGGDGEEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL  
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTR LGT  
YYNSSSVYSFGEGPLTCFFWFILQIPEHRRMLLSPEVVQALLVEELLSTVNSSAAVPYRAEY  
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGQVLRLKGPDHLASSCLWHLQGPKDLML  
KLRLEWTLAECRDLRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY  
YDPFVLSVQPVVFQACEVNLTLNRLDSQGVLSPTYFPSYSPQTHCSWHLTVPSLDYGLAL  
WFDAYALRRQKYDLPCTQGQWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP  
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS  
LPKVCDCGQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKKPNPQCDGRPD CRDGSDEEHCD  
CGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIADRWVITA AHCFQEDSMAS TVL  
WTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA  
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG  
KKDACQGDSSGGLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIIQQVVT

### Important features:

#### Type II transmembrane domain:

amino acids 46-67

#### Serine proteases, trypsin family, histidine active site.

amino acids 604-609

#### N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447  
and 509-512

#### Kringle domains.

amino acids 746-758 and 592-609

#### Homologous region to Kallikrein Light Chain:

amino acids 568-779

#### Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

## FIGURE 64

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC  
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT  
CTCCCTCACCGGGCCCCGGTGTGCGGGTGCACTATGGCTTGTACAACCAGTCGGACCCCTGCC  
CTGGAGAGTTCTCTGTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC  
TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGA  
CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG  
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGG  
AGCTGCGTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCGACTGCAGGGACGGCTCGGA  
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT  
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCTGGGGTCGACACATCTGTGGG  
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT  
GGCCTCCACGGTGCTGTGGACCGTGTTCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG  
GAGAGGTGTCCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT  
GACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCCTCGGCCGCCGTGCGCCC  
CGTCTGCCTGCCCCGCGCGCTCCCACTTCTTCGAGCCCGGCCTGCACTGCTGGATTACGGGCT  
GGGGCGCCTTGCGCGAGGGCGGCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG  
ATCCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC  
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTGAGGGTGACTCAGGTGGTCCGCTGGTGTGCA  
AGGCACTCAGTGGCCGCTGGTTCTGGCGGGGCTGGTCAGCTGGGGCCTGGGCTGTGGCCGG  
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT  
GACCTGAGGAACTGCCCCCTGCAAAGCAGGGCCACCTCCTGGACTCAGAGAGCCCAGGGC  
AACTGCCAAGCAGGGGGACAAGTAT

09078299-101504  
F05T0T" 55282660

## FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG  
CTCCGTGCCGCCAAGTTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCCAGCCCCCTGGCCG  
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAAACACCAAGAGGTGGTTTTTTGTTTTTTAAA  
ACTTCTGTTTCTTGGGAGGGGGTGTGGCGGGGCAGGATGAGCAACTCCGTTCTCTGCTCTG  
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC  
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG  
TTTAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTCGGCCACAG  
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAACCTTTTTTCATCATTACGGAT  
GGACGATGAGCGGTATCTTTGAAAACCTGGCTGCACAACTCGTGTCAGCCCTGCACACAAGA  
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCACCAGCTTTACACGGA  
TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG  
AGAAGGACGATTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG  
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGC  
CGGGCCCATGTTTGAAGGGGCCGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTG  
TGGATGTCCTCCACACCTACACGCGTTCCTTCGGCTTGAGCATTGGTATTGAGATGCCTGTG  
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT  
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAAATGTGAGCATGAGCGAGCCG  
TCCACCTCTTTGTTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTGCCTTCCAGTGCACT  
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT  
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG  
CAGGCATGCCTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA  
CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCA  
CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGCATGTCCTAGGAAAGGGAATCTTT  
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

0978299-101501

## **FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRRTSKDPEHE  
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWL  
PLAHQLYTDVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGT  
GRITGLDPAGPMFEGADIAHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF  
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLQNQDKPSFAFQCTDSNRFKKGICLS  
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Lipases, serine active site.**

amino acids 163-172

#### **N-glycosylation sites.**

amino acids 80-83 and 136-139

09976299.101501  
T05101"65284660

# FIGURE 67

CGGACGCGTGGGCGGACGCGTGGGCCTGGGCAAGGGCCGGGGCGCCGGGCCGAGCCACCTCTTCCCCCTCCCCCG  
TTCCCTGTGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGCTGACAGT  
CGGCAAAGTTTGGCCCCGAGAGGAAGTGGTCTCAAACCCCGGAGGTGGCGACCAGGCCAGACCAGGGGGCGCTCG  
CTGCCCTGCGGGCGGGCTGTAGGCGAGGGCGCGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG  
AGAAGAGTGCGGCGGCGGACGGAGAAAACTCCAAAGTTGGCGAAAGGCACCGCCCCCTACTCCCGGGCTGCCG  
CCGCCCTCCCCGCCCCAGCCCTGGCATCCAGAGTACGGGTGAGCCCGGGCCATGGAGCCCCCTGGGGAGGCGG  
CACCAGGAGCCTGGGCGCCCCGGGGCTCCGCCGCGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCCTCCG  
GCACCTCTGGACAGCCAGGATGCTGTTGGCCACCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG  
ACCGGATTATTTTCCAAATCATGCTTGTGAGGACCCCCAGCAGTGCTCTTAGAAGTGAGGGCACCTTACAGA  
GGCCCCCTGGTCCGGGACAGCCGACCTCCCCTGCCAACTGCACCTGGCTCATCCTGGGCAGCAAGGAACAGACTG  
TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCCCTACGCTCCCCCTCTCCAGCCAC  
TGATCTCCCTGTGTGAGGCACCTCCCAGCCCTCTGCAGCTGCCCGGGGGCAACGTCAACATCACTTACAGCTATG  
CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCTGCTCTCCTACAGCCAAGATTGGCTGATGTGCCCTGCAGGAAG  
AGTTTCAGTGCCCTGAACCAACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCCTGTGGCGATGGCT  
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCCCCTCCCTGCCCTTGCAATG  
TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTAGCCTCAGTCTCCACCCCCAGT  
CCTGCCATTGGCTGCTGGACCCCCATGATGGCCGGCGGCTGGCCGTGCGCTTACAGCCCTGGACTTGGGCTTTG  
GAGATGCAGTGATGTGTATGACGGCCCTGGGCCCCCTGAGAGCTCCCGACTACTGCGTAGTCTCACCCACTTCA  
GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGCTTACCACACAGTTGCTTGGAGCA  
ATGGTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCCTTGGGACAGACCCTGTGGCTTAGGGCT  
CTGGCCTGGGAGCTGGCGAAGGCCTAGGTGAGCGCTGCTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACT  
GTGCTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCCCTGTGGGGCTGCTGGCACCT  
CTGGTGCCACAGCCTGCTACCTGCCTGCTGACCGCTGCAACTACCAGACTTCTGTGCTGATGGAGCAGATGAGA  
GACGCTGTGCGCATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCGTGTATGAGACGTGGGTGTGCG  
ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTCAATACAG  
CTGCAGTCAATTGGCAGCCTAGTGTGCGGCTGCTCCTGGTCACTCGCCCTGGGCTGCACCTGCAAGCTCTATGCCA  
TTCGCACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCC  
CTTCCTACGGGCAGCTCATTGCCAGGGTGCCATCCCACCTGTAGAAGACTTTCCTACAGAGAATCCTAATGATA  
ACTCAGTGCTGGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCAGGTG  
CCCGCGTCTGTCAGCGGGGCGCTTGATGCGACGCTGGTACGCCGTCTCCGCCGCTGGGGCTTGCTCCCTCGAA  
CCAACACCCCGGCTCGGGCCTCTGAGGCCAGATCCCAGGTACACCTTCTGCTGCTCCCCCTTGGAGCCCTAGATG  
GTGGCACAGGTCCAGCCCGTGAGGGCGGGGAGTGGGTGGGCAAGATGGGGAGCAGGCACCCCCACTGCCCATCA  
AGGCTCCCCCTCCATCTGCTAGCACGTCTCCAGCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC  
TGCCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGAGGCCCTGCGAGGCCGCTGTTGCCCCAGCCTGGGGCCCC  
CAGGACCAACCCGGAGCCCCCTGGACCCACACAGCAGTCTTGGCCCTGGAAGATGAGGACGATGTGCTACTGG  
TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGG  
CTCTACTGAGGCCTCTCCCCTGGGGGCTCTACTCATAGTGGCACAACCTTTTAGAGGTGGGTGAGCCTCCCCCTCC  
ACCACTTCTTCCCTGTCCCTGGATTTAGGGACTTGGTGGGCCTCCCGTTGACCCTATGTAGCTGCTATAAAGT  
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCAGTCCCT  
TCACCACCACCTGCTCCCCACGCCACACCATTTGGGTGGCTGTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA  
GGTCTGGACACTCCATCCTTGCCAAACCTTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAAGTAGAGA  
CCCTCCAGCCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTTGCCATCCACAATCCCTCTACAGGGCCTGG  
CTCACAAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA  
GGAATCATACATCTC

09978299.101501



## FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTLQRPLVRDSRTSPANCTWLIL  
GSKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAP  
MGQGFLLSYSQDWLMCLQEEFQCLNHRCVSAVQRCDGVDACGDGSDEAGCSSDPFPGLTPRP  
VPSLPCNVTLEDIFYGVFSSPGYTHLASVSHPOQCHWLLDPHDGRRLLAVRFTALDLGFGDAVH  
VYDGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLP  
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGAT  
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRRCRDEKCVYETWVCDGQPD CADGSDEWDCS  
YVLPRKVITA AVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY  
GQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQRGRLMRRLVR  
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKA  
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLPSLPGPPGPTRSPPGPHTAV  
LALEDEDDVLLVPLAEPGVWVAEAEDEPLLT

### Important features:

#### Signal peptide:

amino acids 1-16

#### Transmembrane domain:

amino acids 442-462

#### LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

0978299.101501

## FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG  
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA  
GACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGG  
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC  
AAGCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATA  
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATAT  
TATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG  
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT  
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA  
GCCTGTGCATGAAAAAAAAAGAAGTTTTGTAATTTTATATTACTTTTTAGTTTGATACTAAGT  
ATTAAACATATTTCTGTATTCTTCCAAAAAAAAAAAAAAAAAAAA

09978299.101501  
T05101 6528260

## FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645

><subunit 1 of 1, 152 aa, 1 stop

><MW: 17170, pI: 9.62, NX(S/T): 1

MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTFFIIAQAPEPYIVITGFEVTVILFFILL  
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTTLTVGGGVFALVTAVCCLAD  
GALIYRKLLFNPSGPYQKKPVHEKKEVL

### **Important features:**

#### **Potential type II transmembrane domain:**

amino acids 26-42

#### **Other potential transmembrane domain:**

amino acids 44-65, 81-101 and 109-129

#### **Leucine zipper pattern**

amino acids 78-99 and 85-106

#### **N-myristoylation site.**

amino acids 110-115

#### **Ribonucleotide reductase large subunit protein**

amino acids 116-127

09978299-10150  
TOSTOT-5528/650

## FIGURE 71

GGGCGAGAAGTAGGGGAGGGCGTGTTCCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC  
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA  
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG  
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAAGCCCC  
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTTCATACTTTTAT  
ATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATATTATCAAC  
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC  
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTNTTGCCGAC

09978299.101501

## FIGURE 72

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG  
CTGGGCGCGCCCCCGGGCCCCCGCGTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC  
CTCTGCTGGCCCAGTGGCTCCTGCGCGCCGCCCCGGAGCTGGCCCCGCGCCCTTCACGCTG  
CCCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCACCCCGGGACCCGGGACCC  
TGCCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG  
GCGCCGCCAACTTCTTGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC  
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG  
TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT  
CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG  
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAA  
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATAC  
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC  
CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC  
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT  
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG  
AAATTGGAATTTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC  
CATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG  
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCAG  
CTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT  
GAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTACG  
CCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCATCCACAAAT  
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAA  
GAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT  
CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG  
CCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT  
AATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCA  
ATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA  
CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG  
CTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCTGTCTCCAGATGCCTTCTAGATTAC  
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA  
AAAAAAACTTCATTCTAA

09973299.101501

## **FIGURE 73**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493

><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTTPGPGTPAERHADGLAL  
ALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS  
YIDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENF  
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS  
LVLGGIEPSLYKGGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLR  
LPQKVFDVAVEAVARASLIPEFSDGFWTGSQLACWTNSETPWSYFPKISIIYLRDENSRSRFR  
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA  
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLIVLLLLPFRCL  
QRRPRDPEVVNDESSLVRHRWK

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 466-494

#### **N-glycosylation sites.**

amino acids 170-173 and 366-369

#### **Leucine zipper pattern.**

amino acids 10-31 and 197-118

#### **Eukaryotic and viral aspartyl proteases**

amino acids 109-118, 252-261 and 298-310

09078299.101501  
T05T01" 65284660

## FIGURE 74

CGCCTCCGCCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG  
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGCCCTGGGCGGGAGCCGGGAGGCGCGGCC  
GGCATGGAGGCGCTGCTGCTGGGCGCGGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA  
CAACCTGGTGAAGGCCCGCCGTGCGGCGGCATGGGCAACCTGCGGGGCGGCACGGCCGTGG  
TCACGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG  
CGCGTGGTGTGCTGGCCTGCCGACCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA  
GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC  
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC  
GGTATCAGTTCCTGTGGCCGGACCCGTGAGGCGTTTAACCTGCTGCTTCGGGTGAACCATAT  
CGGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCTGAAGGCATGTGCCCTTAGCCGCG  
TGGTGGTGGTAGCCTCAGCTGCCCCTGTCGGGGACGTCTTGACTTCAAACGCCTGGACCGC  
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT  
GTTTGCCCGGGAGCTCGCCAACCAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCCACC  
CAGGGCCTGTGAACTCGGAGCTGTTCTGCGCCATGTTCTTGATGGCTGCGCCCACTTTTG  
CGCCCATTTGGCTTGGCTGGTGCTCCGGGCACCAAGAGGGGGTGCCAGACACCCCTGTATTG  
TGCTCTACAAGAGGGCATCGAGCCCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGGAAG  
AGGTGCCTCCAGCTGCCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG  
CTGGCAGGGCTTGGGCCTGGGGAGGATGCTGAACCCGATGAAGACCCCCAGTCTGAGGACTC  
AGAGGCCCCATCTTCTCTAAGCACCCCCACCCTGAGGAGCCCACAGTTTCTCAACCTTACC  
CCAGCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG  
CCTGAGATCCAGCTCTCCTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCTT  
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC  
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAAT  
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT  
AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATTCTG  
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG  
TGAACCTGATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCCATGTTAATGAAGCG  
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG  
GGATCTGAACCCAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA  
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCCATGGGAGTAAGGGGACGCCTTCGGGGCGG  
ATGCAGGGCTGGGGTCACTGTATCTGAAGCCCCTCGGAATAAAGCGCGTTGACCGCCAAAA  
AAAAAAAAAAAAAAAAAAAA

097829.10501

## **FIGURE 75**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGAAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSIGIGKMTALELARRGAR  
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG  
ISSCGRTREAFNLLLRVNHIGPFLLTHLLLPCLKACAPSRVVVASAAHCRGRLDLDFKRLDRP  
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPVNSELFLRHVPGWLRPLLR  
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDRAAHLWEASKRL  
AGLGPGEDAEPDEDPQSEDSEAPSSLSTPHPEEPTVSQPYPSPOSSPDLSKMTHRIQAKVEP  
EIQLS

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Glycosaminoglycan attachment site.**

amino acids 46-49

#### **Short-chain alcohol dehydrogenase family**

amino acids 37-49 and 114-124

09978299.101501  
TOSTOT 66287650



# FIGURE 76

GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATGGGAGGCATGGCTCAG  
 GACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGC  
 CAAGCCTCAGGCCAGGCCACCTCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCCTGAGCATGGTGCCCCCAGAC  
 CCACACCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCACGATGGCCAG  
 GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGCGCT  
 CGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAG  
 TTTACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTG  
 GCCCTCCAGCCCCGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGG  
 ACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGGTTTTCCATCCAGGAGCCC  
 CAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTACAGCTGGAAATGTGACACTGCTGAACCCGGAT  
 CCTGCAGAGGGCCCCAAGCCTAGACCGGCGGTGTGGCTCAGCTGGAAGGTGAGTGGCCCTGCTGCGCCTGCCCAA  
 TCTTACACGGCCTTGTTCAGGACCCAGACTGCCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGGAGCTGCTGGCC  
 GGCTGGCAGAGCGCAGAGCTTGGAGGCCTCCACTGGGGCCAAGACTACGAGTTCAAAGTGAGACCATCCTCTGGC  
 CGGGCTCGAGGCCCTGACAGCAACGTGCTGCTCCTGAGGCTGCCGAAAAAGTGCCAGTGCCCCACCTCAGGAA  
 GTGACTCTAAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCCACCACCTGCTGAAAACCAATGGCATC  
 ATCCGTGGCTACCAGGTCTGGAGCCTGGGCAACACATCACTGCCACCAGCCAAGTGGACTGTAGTTGGTGAGCAG  
 ACCCAGCTGGAAATCGCCACCCATATGCCAGGCTCCTACTGCGTGCAAGTGGCTGCAGTCACTGGTGTGGAGCT  
 GGGGAGCCAGTAGACCTGTCTGCCTCCTTTTAGAGCAGGCCATGGAGCGAGCCACCCAAGAACCCAGTGAGCAT  
 GGTCCCTGGACCTGGAGCAGCTGAGGGCTACCTTGAAGCGGCTGAGGTCAATTGCCACCTGCGGTGTGGCATC  
 TGGCTGCTGCTTCTGGGCACCGCGTGTGTATCCACCGCGGCGGAGCTAGGGTGCACCTGGGCCCCAGGTCTG  
 TACAGATATACAGTGAGGATGCCATCCTAAAACACAGGATGGATCACAGTGACTCCAGTGGTTGGCAGACACT  
 TGGCGTTCCACCTCTGGCTCTCGGGACCTGAGCAGCAGCAGCAGCCTCAGCAGTGGCTGGGGGCGGATGCCCGG  
 GACCCACTAGACTGTCTGCTCCTTGTCTCCTGGGACTCCCGAAGCCCCGGCGTGCCCCCTGCTTCCAGACACC  
 AGCACTTTTTATGGCTCCCTCATCGCTGAGCTGCCCTCCAGTACCCAGCCAGGCCAAGTCCCCAGGTCCCAGCT  
 GTCAGGCGCCTGCCACCCCAGCTGGGCCAGCTCTCCAGCCCCCTGTTCCAGCTCAGACAGCCTCTGCAGCCGCGAGG  
 GGACTCTCTTCTCCCCGCTTGTCTCTGGCCCCCTGCAGAGGCTTGAAGGCCAAAAAGAAGCAGGAGCTGCAGCAT  
 GCCAACAGTTCCCCACTGCTCCGGGGCAGCCACTCCTTGGAGCTCCGGGCTGTGAGTTAGGAAATAGAGGTTCC  
 AAGAACCTTTCCCAAAGCCAGGAGCTGTGCCCCAAGCTCTGGTTGCCTGGCGGGCCCTGGGACCGAAACTCCTC  
 AGTCTCTCAAATGAGCTGGTTACTCGTCACTCTCCCTCCAGCACCCCTCTTCTCTCATGAAACTCCCCCACTCAG  
 AGTCAACAGACCCAGCCTCCGGTGGCACCACAGGCTCCCTCCTCCATCCTGCTGCCAGCAGCCCCCATCCCCATC  
 CTTAGCCCCCTGAGTCCCCCTAGCCCCCAGGCCTCTTCCCTCTCTGGCCCCAGCCAGCTTCCAGTGGCTGTCC  
 AGTCTCTCACTGTCTATCCCTGGGGGAGGATCAAGACAGCGTGTGACCCCTGAGGAGGTAGCCCTGTGCTTGGAA  
 CTCAGTGAGGGTGAGGAGACTCCAGGAACAGCGTCTCTCCCATGCCAAGGGCTCCTTACCCCCCACCACCTAT  
 GGGTACATCAGCGTCCCAACAGCCTCAGAGTTACGGACATGGGCAGGACTGGAGGAGGGGTGGGGCCCAAGGGG  
 GGAGTCTTGCTGTGCCACCTCGGCCCTGCCTCACCCCCACCCCCAGCGAGGGCTCCTTAGCCAATGGTTGGGGC  
 TCAGCCTCTGAGGACAATGCCGCCAGCGCCAGAGCCAGCCTTGTGAGTCTCTCCGATGGCTCCTTCTCTCGTGT  
 GCTCACTTTGCCCGGGCCCTGGCAGTGGCTGTGGATAGCTTTGGTTTTCGGTCTAGAGCCCAGGGAGGCAGACTGC  
 GTCTTTCATAGATGCCTCATCACCTCCCTCCCCACGGGATGAGATCTTCTTGACCCCCAACCTCTCCCTGCCCTG  
 TGGGAGTGAGGGCCAGACTGGTTGGAAGACATGGAGGTGAGCCACACCCAGCGGTGGGAAGGGGGATGCCTCCC  
 TGGCCCCCTGACTCTCAGATCTCTTCCAGAGAAGTCACTGCTGATGCCAAGGCTGGTGTCTTCTCCT  
 GTAGATTACTCTTGAACCGTGTCCCTGAGACTTCCAGACGGGAATCAGAACCCTTCTCCTGTCCACCCACAAG  
 ACCTGGGCTGTGGTGTGGGTCTTGGCCTGTGTTTCTCTGCAGCTGGGGTCCACCTTCCCAAGCCTCCAGAGAG  
 TTCTCCCTCCACGATTGTGAAAACAAATGAAAACAAATTAGAGCAAAGCTGACCTGGAGCCCTCAGGGAGCAAA  
 ACATCATCTCCACCTGACTCCTAGCCACTGCTTTCTCCTCTGTGCCATCCACTCCACCACCAGGTTGTTTTGGC  
 CTGAGGAGCAGCCCTGCCTGCTGCTCTTCCCCCACCATTGGATCACAGGAAGTGGAGGAGCCAGAGGTGCCTTT  
 GTGGAGGACAGCAGTGGCTGCTGGGAGAGGGCTGTGGAGGAAGGAGCTTCTCGAGCCCCCTCTCAGCCTTACCT  
 GGGCCCCCTCCTCTAGAGAAGAGCTCAACTCTCTCCCAACCTCACCATGGAAGAAAAATAATTATGAATGCCACTG  
 AGGCACTGAGGGCCCTACCTCATGCCAAACAAAGGGTTCAAGGCTGGGTCTAGCGAGGATGCTGAAGGAAGGGAGG  
 TATGAGACCGTAGGTCAAAGCACCATCCTCGTACTGTTGTCACTATGAGCTTAAGAAATTTGATACCATAAAAT  
 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

09978299.101501

## **FIGURE 77**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404

<subunit 1 of 1, 985 aa, 1 stop

<MW: 105336, pI: 6.55, NX(S/T): 7

MGGMAQDSPPQILVHPQDQLFQGGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLLP  
DGTLLLLQPPARGHAHDGQALSTD LGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM  
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEGTYMCV  
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTLLNPDPAEGPKPRPAVWLSWKV  
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG  
PDSNVLLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP  
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGWP  
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD  
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST  
FYGSLIAELPSSTPARPSPQVPAVRRLLPPQLAQLSSPCSSSDSLCSRRGLSSPRLSLAPAEA  
WKAKKKQELQHANSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS  
SSNELVTRHLPPAPLFPHPETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPSPQASS  
LSGPSPASSRLSSSSSLSSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY  
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPRPCLTPTPSEGLANGWGSASEDNAASARA  
SLVSSSDGSFLADAHFARALAVAVDSFGFGLEPREADCVFIDASSPPSPRDEIFLTPNLSLP  
LWEWRPDWLEDMEVSHTQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGASPV DYS

### **Important features:**

#### **Transmembrane domain:**

amino acids 448-467

#### **N-glycosylation sites:**

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

#### **N-myristoylation sites.**

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

#### **Phosphotyrosine interaction domain proteins**

amino acids 740-753

0978299.101501  
TOSTOT 65282660

# FIGURE 78

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCT  
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT  
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT  
 GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT  
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCCTGTGGA  
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGGCCCCGATGAG  
 TCTTTACTGATCTCTCTGTTTCGTCTTTCCAGGACCCTGCTGTCTCTCCCTCCCCTTCTCCAC  
 CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCC  
 CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG  
 GCTGAGGCCCCCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC  
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCCATGCAGC  
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG  
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCCCTGGTGTCTGCTGAGCCTTCTGTGAGC  
 CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA  
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCC  
 CCTTCCCAGGCCCCCTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA  
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT  
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG  
 TCCAGCTGCCCCGACTCCAGGGCTCTCCCCACCCTCCCAGGCTCTCCTCTTGATGTTCCA  
 GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG  
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA  
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCCTGGGC  
 CTCATGCCCAGTGTGCGACCCTGCCTTCTCCCACTCCAGACCCACCTTGTCTTCCCTCCC  
 TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGTGATGAAGAGGAGCATGCT  
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT  
 GTGAAAAACGTGATTCTGGCCCCACCAAGACCACCAAAACCATCTCTGGGCTTGGTGCAG  
 GACTCTGAATTCTAACAATGCCAGTACTGCTGAGTTTCAATCTGCCAGGAACCTCCTGGGC  
 ATGAACGCTCACACCCCTCAGCTTAGACTCTGCATTTGGGCTGTGAGCTCTCCACCTGCCC  
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCTGCTAAG  
 TCCAGGCCTTGGTCAGGTGAGGTGCACATTGCAGGATAAGCCCAGGACCCGGCACAGAAGTGG  
 TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCCCTTTGGAAAAAATGATGAAGA  
 AAACCTTGGCTCCTTCCCTTGTCTGGAAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA  
 GAAAAGTAGAAAACCAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG  
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA  
 GCACAACTACTATTTTTTTTTCTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT  
 GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACCTCCGCTCCTGGGTTCAAGTGATT  
 CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT  
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCCTGAC  
 CTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG  
 TCTGGCCCTATTTCTTTTAAAAAGTGAAATTAAGAGTTGTTTCAAGTATGCAAACTTGGAAG  
 ATGGAGGAGAAAAAGAAAGGAAGAAAAAATGTACCCATAGTCTCACCAGAGACTATCAT  
 TATTTCTGTTTTGTTGTACTTCCCTTCCACTCTTTTCTTCTTACATAATTGCCGGTGTCTT  
 TTTACAGAGCAATTATCTTGTATATACAACCTTTGTATCCTGCCTTTTCCACCTTATCGTTCC  
 ATCACTTTATTCCAGCACTTCTCTGTGTTTTACAGACCTTTTATAAATAAAATGTTTCATCA  
 GCTGCATAAAAAAAAAAAAAA

09978299 101501

## FIGURE 79

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS  
GTIYAE EEGQETMKGRVSIRDSRQELSLIVTLWNLTLDAGEYWCGVEKRGPD ELLISLFV  
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQKGTGAEAPPLPG  
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI  
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAE EKEAPSQAPEGD  
VISMPPLHTSEEEELGFSKFVSA

### **Important features:**

#### **Signal peptide:**

amino acids 1-17

#### **Transmembrane domain:**

amino acids 248-269

#### **N-glycosylation site.**

amino acids 96-99

#### **Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

#### **Ig like V-type domain:**

amino acids 13-128

00078299.101501  
TOSTOT" 66282660

## FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA  
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC  
GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT  
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA  
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAA  
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG  
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTGTTGGCCCTGGTCTGTCTGC  
TCAGCTGCCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG  
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC  
TTATTTACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA  
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCCAAC  
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC  
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTACTGGGAGGCCTGGAGGCATCACTGCC  
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA  
CAGCAGGCTGGGAAATGTGGTTTGGTTCCTGACCTAGGCTTGGAAGACAAGCCAGCGAATA  
AAGGATGGTTGAACGTGAAA

0978299-101501

## FIGURE 81

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD  
YEADGSTNNGIFQINSRRWCSNLTNPVNPVCRMYSDDLNPNLKDTVICAMKITQEPQGLGY  
WEAWRHHCQKDLTEWVDGCDF

### **Important features:**

#### **Signal peptide:**

amino acids 1-18

#### **N-myristoylation site.**

amino acids 67-72

#### **Homologous region to Alpha-lactalbumin / lysozyme C proteins.**

amino acids 34-58 (catalytic domain), 111-132 and 66-107

09078299-101501  
TOPOT 65282660

## FIGURE 82

AGCCGCTGCCCCGGGCGGGCGCCCGCGGCGGCACCAATGAGTCCCCGCTCGTGCCTGCGTTC  
GCTGCGCCTCCTCGTCTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCA  
AGCTGTCGTCCGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATC  
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC  
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCGGAACCGGCGCTGGAAGTGCTCCACAC  
TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTG  
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGACGAGTGGGGAGCT  
GGAGAAGTGCGGCTGTGACAGGACAGTGCATGGGGTCAGCCACAGGGCTTCAGTGGTCAG  
GATGCTCTGACAAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG  
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG  
GAAGGCCATCCTGACACACATGCGGGTGGAATGCAAGTGCCACGGGGTGTCAGGCTCCTGTG  
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCGCCAGGTGGGTACGCACTGAAGGAG  
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACC  
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG  
ACTTCTGTGAGCAGGACATGCGCAGCGGCGTGCTGGGCACGAGGGGGCCGCACATGCAACAAG  
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGCGGCTTCACACGGCGCA  
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCACCTGGTGCTGCTTCGTCAAGTGCCGGC  
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGAACCGCCTGCCTAGCCCTGCGCCGGC  
AACCACCTAGTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCCACCACCTACCCCAAGA  
GATACTGGTTGTATTTTTTGTCTGGTTTGGTTTTTGGGTCTCATGTTATTTATTGCCGAA  
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAAGCCTGGGCCTTTGTGGCT  
GCCACTGACCAAAGGGACCTTGCTCGTGCCGCTGGCTGCCC GCATGTGGCTGCCACTGACCA  
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTAT  
TACCACCACATGGCTACTGACCGTGTATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATA  
GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAAGTCTCCAGCACACA  
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG  
GAACAAGCAGATACCAGGTCAAGGGCACCAAGGTTCATTTACGCCCTTACATGGACAGCTAGA  
GGTTCGATATCTGTGGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA  
GTCCCACCCTAGAACCCAGCCTGCCCCAGCCTGCCCCCTGGGAAGAGGAACTTAACCACTCC  
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT  
TGCAGTCATGCCCGAGTCACCTTTACAGCGCTGTTCTCCATGAACTGAAAAACACACAC  
ACACACACACACACACACACACACACACACACACACACACACACACACACCTGCGAGA  
GAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCGAGTCACCTTTACAGCACTGTTCTC

09978299.101501

## **FIGURE 83**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNLE  
VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLVPFGKVVTQGTREAAFVYAISSAGVAFV  
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFDVVRERSKGASSSRALM  
NLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR  
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC  
CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation sites.**

amino acids 88-91 and 297-300

#### **Wnt-1 family signature.**

amino acids 206-215

#### **Homologous region to Wnt-1 family proteins**

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

00978299-101501  
T05T0T 65282660



## FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT  
CGCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC  
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTC  
ACCACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC  
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGCGCTGG  
GTGCCCTGAAGGAGGAGGTTCGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG  
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT  
GCGGGAACCTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGGCCGTGAGGACG  
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCCTGCGAGCCG  
TGCCCCACGTCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC  
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC  
TGGATGAGCAGGGCTTCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGG  
GCTGTGCGCCATCTGGGCAAGGTTCAAGGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTT  
CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTCTATGATGC  
TGCACACGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG  
AAAAGGCACAACCTGCTTGACCCCGCCAGTGCCCTGGAGCCGCGCCCATTGCAGCATGTCGTA  
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTCTTCCT  
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC  
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACC  
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA  
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGA  
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAA

## **FIGURE 85**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352

<subunit 1 of 1, 293 aa, 1 stop

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYSKWGSSEEVPGGPWGRVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA  
LLDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALR  
ELRERVTOGLAEAGRGREDVRTELFRALAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTW  
AAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS  
HWNQGEPNDAWGRENVMMLHTGLWNDAPCDSEKDGWICEKRHNC

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 31-54

#### **N-glycosylation sites.**

amino acids 73-76 and 159-162

#### **Leucine zipper pattern.**

amino acids 102-123

#### **N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

#### **C-type lectin domain signature.**

amino acids 264-287

09070299-101504  
TOSTOT" 55284560

# FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG  
 GCAGCCCCCGCCGCCCCCGCAGCCCCCTTCTCCTCTTTCTCCACGTCCTATCTGCCTCTCG  
 CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACTGGAGCCTCATTGGCCGGCCCCGG  
 GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC  
 CGCGCTCCCGCTGCTCCTGCCGGGTGATGGAAAACCCCAGCCCCGGCCGCCCTGGGCAAG  
 GCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTC  
 CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA  
 CGGCCTTCCCCAAGCAGTACCCCCTGTTCCGCCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG  
 GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTCAGTAACGGGCTGCG  
 CGACTTTGCGGAGCGCGGCGAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGGAGG  
 CGCTGCAGAGCGTGACGAGGTGTTTTCGGCGCCCGCCGTCCCCAGCGGCACCGGGCAGACG  
 TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCC  
 CAGCCCCGACTGGTTCTGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG  
 AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTCACCTTCTCC  
 TCCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCTCCCAG  
 CCACCCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA  
 CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCCTGCCCAGC  
 AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTC  
 CCTGTGGTTCGTCTTGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA  
 CTCGCTACGTCCGGGTCCAGCCCGCCAACAACGGGAGCCCCCTGCCCGAGCTCGAAGAAGAG  
 GCTGAGTGCGTCCCTGATAACTGCGTCTTAAGACCAGAGCCCCGCAGCCCCTGGGGCCCCCCC  
 GAGCCATGGGGTGTCGGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCACAGGG  
 GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT  
 CTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG  
 CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC  
 CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCCTTCATCG  
 TCCAGGGGCCTGGCTCCACGTGGTTGCAGATACCTCAGACCTGGTGCTCTAGGCTGTGCTG  
 AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG  
 TTTCCGAAGCGTCAGTGTTTCCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT  
 GTTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

097829.101501

## **FIGURE 87**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL  
FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALMKEIEAAGEALQSVHEVF  
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVSPDWFGVDSLCLCDGDRWREQAALDLYP  
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP  
RAFIPPAPVLPSPRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGR LGTKSRTRYVRVQPA  
NNGSPCPELEEEAECVPDNCV

**Important features:**

**Signal peptide:**

amino acids 1-26

09978299.101501  
F0510T" 66284660

## FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGCGTGA  
TATTGACAAACTGAAGCTTTCCTGCACCACTGGACTTAAGGAAGAGTGTA CTCTGAGGCGGA  
CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC  
CAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAATGGGAAGGTTTTATTGAAAATA  
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCGAGAAATTTT  
ATCCAACCTTTGTTTGAAGCTTATTATGACAATACCATTTTTTCATAGAGTTGTGCCTGGTTT  
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC  
CATTCAAAGATGAATTTCAATTCACGGTTGCGTTTTTAATCGGAGAGGACTGGTTGCCATGGCA  
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTGAGCAGATGAACT  
TAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC  
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAAATAAAAAGCTGT  
GAGGTTTTGTTTAATCCTTTTGATGACATCATTCCAAGGGAAATTAAAAGGCTGAAAAAAGA  
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTTAGTTTACTTT  
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG  
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT  
TGTAAGAAAGTAAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG  
AGCATGATGAATATATTGATGGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAAA  
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC  
AGTCAGCCGCAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAAACGGGAACCTTTAGCAG  
CAAAACAAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAAGAAGTGAAGAGGAAGAA  
GCCCCCTCCAGATGGTGCTGTTGCCGAATACAGAAGAGAAAAAGCAAAAGTATGAAGCTTTGAG  
GAAGCAACAGTCAAAGAAGGGAACCTTCCCGGGAAGATCAGACCCTTGCACTGCTGAACCAGT  
TTAAATCTAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA  
GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGT  
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA  
ATAAAAGAAGGAGGGAAGAAAGCAAAAGCTGATGAGAGAGAAAAAAGAAAGAAGATTAAAAT  
GAGAATAATGATAACCAGAACCTTGCTGGAAATGTGCCTACAATGGCCTTGTAACAGCCATTG  
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTTGTCTGGTTTTG  
AAAAACAATTATCTTGTTTTGCAAATTGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGG  
TACATGTGTTTTTTCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCTCT  
TCCACAAAAA

09978299 "101501

## **FIGURE 89**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919

><subunit 1 of 1, 472 aa, 1 stop

><MW: 53847, pI: 5.75, NX(S/T): 2

MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVPFGFI  
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN  
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPFDDIIPREIKRLKKEK  
PEEEVKKLKPKGTKNFSLLSFGEAAEEEEEEVNRVSQSMKGKSKSSHDLKDDPHLSSVPVV  
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKSV  
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEEAPPDGAVA EYRREKQKYEALRK  
QQSKKGTSREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMSHVLQFEDKSRKVK  
DASMQDSDTFEIYDPRNPVNKRREESKKLMREKKERR

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 109-112 and 201-204

**Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.**

amino acids 49-66

**Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase**

amino acids 96-140, 49-89 and 22-51

09978299.101501  
TOSTOT"66284560

# FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGG  
 CCCGCCCTCGGCTTTGAGGCGAGAGAAAGTGTCCCAGACCCATTTTCGCCTTGCTGACGGCGTGC  
 AGCCCTGGCCAGACATGTCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC  
 GTGGCCGCCGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAA  
 CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTG  
 CTCCTTCAAGTGGTTTTTGGAAACGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA  
 GGAGGAACAAATACAGGTGCCTTGACACCAAGAGGCCCTCAAGTGGTCACCAAATATGGAAC  
 CCTGCAAGGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTTAGGAGTCCCCT  
 TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAGCCCTGGAAA  
 GGAATCAGAGATGCTACCACCTACCCGCCTGGATGGAGTCTCGCTCTGTGCGCCAGGCTGGAG  
 TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGAGTCTCCTGC  
 CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCG  
 ATGTACGTACGACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT  
 GAACGTGTACGCGCCGCGCGCGCGCCCGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCC  
 CGGGAGGCGCCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCGC  
 GAGAAAGTGGTGCTGGTGTCTGTCAGCACAGGCTCGGCATCTTCGGCTTCTTGAGCACGGA  
 CGACAGCCACGCGCGCGGGAACCTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC  
 AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTTCGGCCAGTCGGCG  
 GGGGCCATGAGCATCTCAGGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGGC  
 CATTTCCAGAGTGGCACCGCGTTATTACAGACTTTTCATCACTAGTAACCCACTGAAAGTGG  
 CCAAGAAGGTTGCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC  
 CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTTCCAAC  
 TGAATTCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG  
 TGATCCCAGATGACCTTTGGTGCTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT  
 CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCTTATAATATACCAAGGAGCAGGT  
 ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA  
 ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCAC  
 TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA  
 AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGC  
 TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC  
 TATGCAGGAAGGAGCCAAAGAGGGGTTTGCCTCCACCATCCAGGCCCTGGGGAGACTAGCCA  
 TGGACATACCTGGGGACAAGAGTTCTACCCACCCAGTTTAGAACTGCAGGAGCTCCCTGCT  
 GCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGTTGTGTGGGACCTGCACTGCCCTTTCCAGCC  
 TGACATCCCATGATGCCCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC  
 ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTTTCCCTTCTTCAAATCCT  
 CCCACCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTCGACCCAGACTGCCACTGC  
 CCCTGTCACTGCACCCAGCTTGGCATTACCATCCATCCTGCTCAACCTTGTTCTGTCTGT  
 TCACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACCTTTGGTAGTTTGGGA  
 TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCCAAAGTCTATACACAGGGGTGG  
 TCTCTTCAATAAAGAAGTGTTGATTAGAAAAA

09973299 " 101501

## FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTAPSSG  
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTQKGQMHVGKTPIQVFLGVPPFSRPP  
LGILRFAPPEPPEPWKGIRDATTPPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS  
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVIYAPARAPGDPQLPVMVWFPGGAF  
IVGAASSYEGSDLAAREKVVLVFLQHRLLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA  
AFGGDPGNVTFLFGQSAGAMISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA  
HLAGCNHNSTQILVNCRLRALSCTKVMRVSNNKMRFLQLNFQRPDEEIIWSMSPVVDGVVIPDD  
PLVLLTQGVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMD  
IVQDATFVYATLQTAHYHRETTPMMGICPAGHATTRMKSTCSWILPQEWA

### **Important features:**

#### **Signal peptide:**

amino acids 1-29

#### **Carboxylesterases type-B serine active site.**

amino acids 312-327

#### **Carboxylesterases type-B signature 2.**

amino acids 218-228

#### **N-glycosylation sites.**

amino acids 318-321, 380-383 and 465-468

09970209 101501  
T05T01 66202660





## **FIGURE 93**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYWFK  
AVTETTTKGAPVATNHQSREVEEMSTRGRFQLTGDPKGNCSLVIRDAQMQDESQYFFRVERGS  
YVTYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS  
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL  
GLELPGVKAGDSGRYTCAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSL  
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP  
LGSQHVLSLSVHYKKGLISTAFSNGAFLGIGITALFLCLALIIMKILPKRRTQTETPRPR  
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP  
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **Transmembrane domain:**

amino acids 399-418

#### **N-glycosylation site.**

amino acids 100-103, 297-300 and 306-309

#### **Immunoglobulins and major histocompatibility complex proteins signature.**

amino acids 365-371

09078299-101501  
TOSTOT" 662826610

# FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAACCTGTTATTTACTGCTGCGTTT  
TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAACAAAGA  
AAGTCAAGCAGCCAGTGCATCTCATTTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT  
TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA  
CAATGGAAACAATTCCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA  
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC  
TACATCTTAAGAGCCCAGGTAAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA  
GTTTGTCTCAAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG  
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT  
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC  
ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC  
TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG  
TCTGGAACAACAAGTGTATTAATTAACTTTTCTAGATGTTAATGACAATAAGCCTATATTTAA  
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA  
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT  
GATTCGCAACATTTGACATTATTACTAATCATGAACTCAAGAAGGAATAGTTATATTTAA  
AAAGAAAGTGGATTTTGTAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAACCATC  
ATGTTCTTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCACTTTCATTAAGATCCAG  
GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTATTTGAAGTTTTTGA  
AGAAACCCACAGGGATCATTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT  
CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCAATATCAATGATAATGGTACAATC  
ACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC  
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCCTGATGTATGTGCAAGTTCTTAACATCA  
AGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT  
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATT  
TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAGTTTACAATCATAGATAATCAAG  
ATAACACAGCTGTCAATTTGACTAATAGAAGTGGTTTTAACCTTCAAGAAGAACCTGTCTTC  
TACATCTCCATCTTAATTTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC  
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG  
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGTCATTATGATCATA  
TTTGGGTTTATTTTTTTGACTTTGGGTTTAAAAACAACGGAGAAAACAGATTCTATTTCTGA  
GAAAAGTGAAGATTTTCAAGAGAGAATATATTCCAATATGATGATGAAGGGGGTGGAGAAGAAG  
ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT  
CGGAAAACCACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA  
CAGTGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG  
CCCCTCCTTTTGATTCCCTCCAGACCTACGCTTTTGGGGAACAGGGTCATTAGCTGGATCC  
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT  
GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTCTGCAGTGCAGTCAAATAATTAGG  
GCTTTTTTACCATCAAAATTTTTAAAAGTGCTAATGTGTATTGCAACCCAATGGTAGTCTTAA  
AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC  
CTGGAGTAAATACTCCATGGTTATTTTAAAGCTACCTACATGCTGTCTTGAACAGAGATGTG  
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTGAAAGTAAATAATG  
TAGGAAGATATTTAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT  
CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAATTTAAAGGAGCAAAAATTTG  
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA  
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCATGAAGTATTGTTTCCTTTAT  
TTAAA

## FIGURE 95

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKGWVWNQFFVPEEMNTTSHH  
IGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT  
GRAVEPESEFVIKVSNDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL  
LYSLLQGQPYFSVEPTTGIVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSD  
VNDNKPIFKESLYRLTVSESAPTGTSTIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE  
TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFL  
PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA  
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR  
DESIEEHFHYFNLSVEDTNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP  
SLTSTNTLTIHVCDGSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIIFGFIFLTGLKQ  
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY  
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESASVSDQD  
ESYDYLNELGPRFKRLACMFGSAVQSNN

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domain:**

amino acids 597-617

#### **N-glycosylation sites.**

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,  
516-519 and 534-537

#### **Cadherins extracellular repeated domain signature.**

amino acids 136-146 and 244-254

097899.10501  
"ESTOT" 66284650

## FIGURE 96

ATTTCAAGGCCAGCCATATTTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTNTA  
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT  
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAA  
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA  
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC  
AGCATTGAAGAGGATGATTGCGCAAACATTTGACATTATT

09978299-101501

# FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCGGGCGCGGACCCCAACCCCGAC  
 CCAGAGCTTCTCCAGCGGGCGGCGCAGCGAGCAGGGCTCCCCGCCTTAACCTTCCCTCCGCGGGG  
 CCCAGCCACCTTCGGGAGTCCGGGTGCCCCACCTGCAAACCTCTCCGCCCTTCTGCACCTGCCA  
 CCCCTGAGCCAGCGCGGGCCCCCGAGCGAGTCAATGGCCAACGCGGGGCTGCAGCTGTTGGGC  
 TTCATTCTCGCCTTCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG  
 GATTTACTCCTATGCCGGCGACAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGA  
 TGTCTTGCCTGTTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT  
 CTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGAT  
 AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGC  
 AGAAGATGAGGATGGCTGTCATTGGGGGTGCGATATTTCTTCTTGAGGTCTGGCTATTTTA  
 GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCCAGT  
 CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCCC  
 TTCTGGGAGGTGCCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCAACACCA  
 AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGTGTGACACAGAGGCAAAAG  
 GAGAAAATCATGTTGAAACAAACCGAAAATGGACATTGAGATACTATCATTAAACATTAGGAC  
 CTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAACAAACAAACAAAAA  
 ACCCATGTGTTAAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTCTCA  
 ATATAGGAGGGAAGATTTTCCATTTGTATTACTGCTTCCCATTTAGTAATCATACTCAAAT  
 GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTTCTATTAAAA  
 ATAGACAGTAAATACTATTCTCATTATGTTGATACTAGCATACTTAAAATATCTCTAAAT  
 AGGTAAATGTATTTAATTCCATATTGATGAAGATGTTTATTGGTATATTTTCTTTTTCGTCC  
 TTATATACATATGTAACAGTCAAATATCATTTACTCTTCTTCATTAGCTTTGGGTGCCTTTG  
 CCACAAGACCTAGCCTAATTTACCAAGGATGAATTCTTTCAATTCTTCATGCGTGCCCTTTT  
 CATATACTTATTTTATTTTACCATAATCTTATAGCACTTGTCATCGTTATTAAGCCCTTAT  
 TTGTTTTGTGTTTCATTGGTCTCTATCTCCTGAATCTAACACATTTCATAGCCTACATTTTA  
 GTTTCTAAAGCCAAGAAGAATTTATTACAAATCAGAACTTTGGAGGCAAACTTTTCTGCATG  
 ACCAAAGTGATAAATTCCTGTTGACCTTCCCACACAATCCCTGTACTCTGACCCCATGCACT  
 CTTGTTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCAGGTGTTGT  
 AACACAACCTTTATTGATTGAATTTTAAAGCTACTTATTTCATAGTTTATATCCCCCTAACT  
 ACCTTTTTGTTCCTTAAATTGATTTGTTTTTCCCAAGTGTAATTATCATGCGTTTTTA  
 TATCTTCCTAATAAGGTGTGCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA  
 ATCTGGTGACAAATATTCTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTTT  
 TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTAA  
 TTAGTTTATATTACTCTTATTCTTTGAACATGAACATATGCCTATGTAGTGTCTTTATTTGCT  
 CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATT  
 CACTGCCTTCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACACACATACCTTCAT  
 GTGGTTCACTGCCTTCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACGCACATAC  
 CTTTCATGTGGCTCAGTGCCTTCCTCTCTCTACCAGTCTATTTCCATTCTTTTCACTGTGTCT  
 GACATGTTTGTGCTCTGTTCCATTTTAAACAACTGCTCTTACTTTTCCAGTCTGTACAGAATG  
 CTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAGACCTG  
 GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGGCAAGGCATTTGGCTGCTGTAA  
 GCTTATTGCTTCATCTGTAAGCGGTGGTTTGTAAATCCTGATCTTCCCACCTCACAGTGATG  
 TTGTGGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAAATTTAAAAAGTGCTAT  
 ACTAAGGGAAAGAATTGAGGAATTAAGTGCATACGTTTTTGGTGTGCTTTTCAAATGTTTGA  
 AAATAAAAAAATGTTAAG

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFI LAFLGWIGAI VSTALPQWRIYSYAGDNIVTAQAMY EGLWMSCVSQSTGQI  
QCKVFDSLNLNLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDDEVQKMRMAVIGGA  
IFLLAGLAILVATAWYGNRIVQEFYDPMTPV NARYEFGQALFTGWAAASLCLLGALLCCSC  
PRKTTSYPTPRPYPKPAPSSGKDYV

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domains:**

amino acids 82-102, 118-142 and 161-187

#### **N-glycosylation site.**

amino acids 72-75

#### **PMP-22 / EMP / MP20 family proteins**

amino acids 70-111

#### **ABC-2 type transport system integral membrane protein**

amino acids 119-133

09978299.101501  
TOSTOT"66282650

## FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC  
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG  
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTTCGAGAGCACCGGGCAG  
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC  
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA  
AGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGC  
GCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN  
CNTTCAACANTTCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCA  
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCT  
GTTCCTGTCCC

09978299.101501



## FIGURE 100

ACCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG  
GCTTCATTCTCCCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG  
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCCAGGCCNTGTACGAGGGGCTGT  
GGATGTCCTGCGTGTCGCGAGGACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT  
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG  
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAGACGATGA  
GGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGACGGTCTGGCTA  
TTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

09978299 .101501

## FIGURE 101

GGGCCCCGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC  
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC  
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTCGCAGANCACCGGGCAGATCCAGTGCAA  
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT  
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT  
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTT  
CTTGCAGGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT  
TCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC  
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTGCGA

09978299.101501

## FIGURE 102

ATTCTCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC  
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT  
GCNTGTCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG  
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC  
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCCAGAAG  
ATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC  
CACAGCATGGTATGGCAATAGANTNNTTCNNGNNNTCTATGACCCTATGACCCAGTCAATG  
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTG  
GGAGGTGCCCTACTTTGCTGTTCTGTCCC

09978299 .101501

## FIGURE 103

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC  
AAGCAACCCCTTGCCCTTGAAGGTGGTTGNCAATCCCCCCTGGGAGTGAATAGCAATCTTTGTG  
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTNNCCACAGCAT  
GGTATGGCAATAGNATNNTTCGNGGNTTCTATGACCCTATGACCCCAGTCAATGCCAGGTAC  
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGC  
CCTACTTTGCTGTTCTGTCCCCGAA

105101" 66282650

## FIGURE 104

AGCAATGCCCTGCCCCCAGTGGAGGATTAATTCCTATGNTGGGGACAACATTGTGACNGCCC  
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGC  
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT  
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGTATGA  
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTT  
CTTNTTGCAAGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTCAAGA  
ATTTTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTNTTCACTG  
GCTGGGCTGCTGCTTNTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTTCCTGCGAACC

09978299-101504  
FOSTOT 65282650

## FIGURE 105

TCATAGGGGGGCGCGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA  
TGGCAATAGAATCGTTCAAGAATTNTATGACCCTATGACCCCAGTCAATGCCAGGTACGAAT  
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA  
CTTTGCTGTTCTG

09978299.101501

## FIGURE 106

TTCCTGGGATGGATCCGCCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC  
TGGCGAACAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC  
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT  
TGCAAGCAACCNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG  
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGNNGCCACAGCAT  
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCTATGACCCCAAGTCAATGCCAGGTA  
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG  
CCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCACG

09978299.101501  
T05T01" 55282660

## FIGURE 107

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA  
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA  
TGTACGAGGGGCTGTGGATGTCNGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCT  
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNTGCCTTGATGGTGGTTGGCA  
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG  
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGC  
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT  
GACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC  
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTCCTGCGAA

09078299 101501  
TOTAL 15284660



# FIGURE 108

GCGTGCCGTCAGCTCGCCGGGCACCGCGGCCCTCGCCCTCGCCCTCCGCCCCCTGCGCCTGCAC  
 CGCGTAGACCGACCCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCGCCCCGTGCCCCG  
 ACCGGTCCCCGCCTTTTTGTAAACTTAAAGCGGGCGCAGCATTAACGCTTCCCGCCCCGGT  
 GACCTCTCAGGGGTCTCCCCGCCAAAGGTGCTCCGCCGCTAAGGAACATGGCGAAGGTGGAG  
 CAGGTCTGAGCCTCGAGCCGACGACGAGCTCAAATTCGAGGTCCCTTCACCGATGTTGT  
 CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTA  
 CAGCACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCCCTCAATT  
 AATGTATCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT  
 TATGGTTTCAGTCTATGTTTGTCTCAACTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG  
 CAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGTTTGAATTGCCAGCAGAGAAT  
 GATAAACCACATGATGTAGAAATAAATAAAATTTATATCCACAACCTGCATCAAAGACAGAAAC  
 ACCAATAGTGTCTAAGTCTCTGAGTTCCTCTTTGGATGACACCGAAGTTAAGAAGGTATGG  
 AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAACAAGCAGTTCAAG  
 GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTACAGCATTAGC  
 CCAACTGGGAAGGAAGAAGGCCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTGTTCTTTA  
 TCGTTGGTGTAAATTATTGGGAAGATTGCCTTGTAAGGTTAGCATGCACAGGATGGTAAATTG  
 GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAATT  
 AATGTATGATGACATCTCACAGGTCTTGCCCTTTAAATTACCCCTCCCTGCACACACATACAC  
 AGATACACACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG  
 ATTGAGGGGGAAAAAGAATGATCTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAAT  
 GGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCCTTGGTACATGATGCTGGATTACCTC  
 TCTTAAATGACACCCCTTCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCCAGCAT  
 GCTGGGGAGTGCGGTGAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTG  
 CTTTCCGTGTCTTCAGTTCGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA  
 AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT  
 TGAATGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAA  
 GCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTGTTATTTCAGAGATGTTTAAATGCATA  
 TTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGC  
 TGCGTGCTGCTGAACCTCTGTTGGGTGAAGTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT  
 GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGTTTTATTGGGATGCTGGAGAAGAGCTGCCA  
 GGAAGTGTTTTTTCTGGGTGAGTAAATAACAACCTGTCATAGGGAGGGAAATTCTCAGTAGTG  
 ACAGTCAACTCTAGGTTACCTTTTTTTAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA  
 CCACCTCTCAACCATTACTCACACTTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC  
 TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC  
 ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTAC  
 TAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGA  
 CTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCCCCAAAATTAAGAAAA

## **FIGURE 109**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHELKFRGPFTDVVTTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGIID  
AGASINVSVMQLQPFDDPNEKSKHKFMVQSMFAPTDTSMEAVWKEAKPEDLMDSKLRVFE  
LPAENDKPHDVEINKIISTTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE  
NKQFKEEDGLRMRKTVQSNPISALAPTGKEEGLSTRLLALVVLFFIVGVIIGKIAL

**Important features:**

**Transmembrane domain:**

amino acids 224-239

**N-glycosylation site.**

amino acids 68-71

**N-myristoylation site.**

amino acids 59-64, 64-69 and 235-240

09978299.101501

## FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG  
GTCCANGTCTGAGCCTGACTTCCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG  
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA  
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA  
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCC  
CCAAAATTAAGAATTCTTTTGTCAATTTGTCACATTTGCTCTATGGGGGGAATTATTATTTT  
ATCATTTTTATTATTTTGCCATTGGAAGGTAACTTTAAAATGAGC

09978299-101501  
F05T0T" 66282660

## FIGURE 111

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT  
AAATGACACCNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG  
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTGCTTT  
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC  
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTA CTGTCATAAGTGAGAGGCGTGTTGA  
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT  
AAATTGTATTGGTTCATGTAGTGAAGTCAAAGTGTATTTCAGAGATGTTTAATGCATATTTA  
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG  
TGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

09078299.101501

## FIGURE 112

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTTGGGAAGATTGCTTGTAGAGGTA  
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT  
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT  
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG  
AAAGTTAAAAATGTATAGTAAC

09978299-101501  
FOSTOT 86282650

## FIGURE 113

GGTGGCCCATTCCTCGGCCAGGCTGCTTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC  
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC  
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT  
GCTTTGTTTANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTG  
TTATTCAGAGATGTTTAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA  
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACTGGTATTGC  
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

0978293.101501

## FIGURE 114

TGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC  
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG  
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC  
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGTGTATTTCAGAGATGTTTAATGC  
ATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA  
TGCTGCGTGC

09978299-101501

## FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAAACCNTGNGT  
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC  
TGGATTACCTCTCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN  
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCANTCCC  
GGCCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA  
ACAGAGTCAGAAGCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA  
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTcantt  
AAAGGGNCCAAGNTAAATTTGTATTGGTTcatGTAGTGAAGTCAAANTGTTATTcAGAGATG  
TTTAATGCATATTTAANTTATTTAATGTATTTcatNTCATGTTTTCTTATTGTCACAAGGGT  
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

09078299 101501  
FOSTOT 65282650



## FIGURE 116

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC  
CACGTGGCCCACTCCCGGCCAGGCTGCTTTCGTGTCTTCAGTTCTGTCCAAGCCATCAGC  
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG  
TACTCGTCATAAGTGAGAGGCGTGTGTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC  
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA  
CTGTTATTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTT  
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTAT  
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

09978299.101501

# FIGURE 117

GCGAGCTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGA  
 GGCTCCCAGCTGCAGCGTCCCCGCCCCGCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC  
 CTCGGGGACCAAAACAAGCCTGGCAGGGTCTCACTTTGTTGCCAGGCTGGAGTTTCAGTGCCA  
 TGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA  
 CTACAGGACAAAATTAGAAGATCAAAATGGAAAAATATGCTGCTTTGGTTGATATTTTTTACC  
 CCTGGGTGGACCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA  
 GGTACCCCGGATTGTCTAGTGAAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATG  
 CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCCAGC  
 CTTTCTGAATTGGAGGATTATCTTTCCTATGAGACTGTCTTTGAGAATGGCACCCGAACCTT  
 AACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG  
 TATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTTCAAGCATCTTGGAACAA  
 AGGTTCTTAACCAATTTCCCTTTTCAAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT  
 TCTCATTTCCCTCAGCATGTTCTAACTGCTGCCCACTGTGTTTATGATGGAAAGGACTATG  
 TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG  
 AAACGTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAAAGAGAGGGTAC  
 CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAAAAATCTGGCCGGGGTC  
 AGAGGATTGCCGAAGGGAGGCCTTCTTTTCAAGTGGACCCGGGTCAAGAATACCCACATTCCG  
 AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA  
 GCTGAAGCGTGCTCACAAAAAGAAATACATGGAACTTGGAAATCAGCCCAACGATCAAGAAAA  
 TGCTGGTGGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT  
 CGGTTTTGTCAGTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC  
 GGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAAGAATTGGAAGC  
 GCAAAATCATTGCGGTCTACTCAGGGCACCAAGTGGGTGGATGTCCACGGGGTTTCAAGAGGAC  
 TACAACGTTGCTGTTTCGCATCACTCCCTTAAATACGCCAGATTTGCCTCTGGATTACAGG  
 GAACGATGCCAATTGTGCTTACGGCTAAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAA  
 TCACAGAGAAAACCAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT  
 GAACTCTGTCAATAGCATTTCACATTTTTTCAAAATCAGGAGATTTTCGTCCATTTAAAAAA  
 TGTATAGGTGCAGATATTGAACTAGGTGGGCACTTCAATGCCAAGTATATACTCTTCTTTA  
 CATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTTCCTTCTTAAAAAATTAGACACACTTT  
 AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC  
 TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAA  
 GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA  
 CTCTGAGATGGATCCATTCAAGCTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT  
 GGGACATTTAGTTTAGTTTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTATAAA  
 CAAAATAATAACTGTTTTTACTGCTTTTAAAGAAATAACAATTACAATGTGTATTATTTAAAAA  
 TGGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTT  
 TAAGATCTCAAGTTTTTTTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG  
 AAGACACTTCACAAATTATGAATGATCATGTGTTGAAAGCCACATTATTTTATGCTATACAT  
 TCTATGTATGAGGTGCTACATTTTTTAGGACAAAGAATTCTGTAATCTTTTTCAAGAAAGAGT  
 CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCTCTGATTAG  
 TAATTTTAGATATGTCCTTTCCTAAAAATGAATAAAATTTATGAATATGA

09978299.101501

## **FIGURE 118**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVC  
GIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV  
YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISPQHVLTAAHCVHDGKDYVKGSKKLRV  
GLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRRKSGRGQRIAEGRPS  
FQWTRVKNTHIPKGWARGMGMDATLDYDYALLELKRAHKKKYMELGISPTIKMPGGMIHFS  
GFDNDRADQLVYRFCSVSDENDLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKIIAVYSG  
HQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **N-glycosylation sites.**

amino acids 90-93, 110-113 and 193-196

#### **Glycosaminoglycan attachment site.**

amino acids 236-239

#### **Serine proteases, trypsin family, histidine active site:**

amino acids 165-170

09978299.104504

## FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT  
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTAGTGTCGGATTCTGATTCCGGCAAGG  
ATCCAAGCAATGGAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC  
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG  
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGAGGGGCCTCCTACTCTCTGAGGCGCT  
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC  
TGCCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA  
CCATGGCCAGTTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA  
AGTGCCAAGCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG  
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGTTTATGCCAAATTGTTGGCTGCGA  
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA  
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACT  
GTGGTTGCACTTCCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAAGGTCTGATCACTT  
ATATCTGGAAACCAAACCCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA  
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA  
ATGGCTGGACCACTCACAGCAGATTTTATTGTCAAGATTCGTAACCTCGGGCTCCGCTGACAG  
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC  
CTTGCTCAGCAACCTGTGGAGGAGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG  
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC  
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC  
CTTATGACCTCTACCATCCCCCTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCC  
TCGTGTGGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCA  
TGTCACCTCAGTGGAAGAGTGGAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT  
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT  
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGCATCGACCATCGAGGAATGCACACAGGAGG  
CTGTAGCCCCAAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA  
AACCCAAAGAGAAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA  
GAAGAAGGAGCTGCTGTGTCAGAGGAGCCCTCGTAAGTGTAAAAGCACAGACTGTTCTATA  
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA  
ACTAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA  
AAAAAAAAA

## FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYSLRRCLS  
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNPCSLKCQ  
AKGTTLVVELAPKVLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR  
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVLKGPDHLYLETKTLQGTKGENSLSSSTGTFL  
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFPACS  
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD  
LYHPLPRWEATPWTACSSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI  
FDCPKWLAQEWSPCTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK  
EKL PVEAKLPWFKQAQEELEGA AVSEEPS

**Important features:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 251-254

**Thrombospondin 1**

amino acids 385-399

**von Willebrand factor type C domain proteins**

amino acids 385-399, 445-459 and 42-56

09078209 101501  
TDETOT 150284650

## FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCCGGTGGGCCCTCGGGCCTGAC  
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG  
GCCCCGCCGTTTCGTGGGGCCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCGGCCTCAT  
GCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGGCCTGGGCCGCGCCACGGCCGCCG  
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCGCCGAGGAG  
GCGGCGGGTCAGCTCCGCCGCGAGCTCCGCCAGGCCGCGGAGTGCGGCCAGAGCCTGGCGT  
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG  
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG  
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA  
TCTGGGGCACTTTCTACTACCAATCTTCTCCTTGACTCCTCAAAAGTTCAGCTCCCAGCA  
GGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC  
AGTGAACAAAGCTATAATAAAAGCTTTTGTATATAGCCGGAGCAAACCTGGCTAACATTCTTTT  
TACCAGGGAAGTAGCCCCGCCGCTTAGAAGGCACAAATGTACCGTCAATGTGTTGCATCCTG  
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC  
AATTTGGTGTCATGGGCTTTTTTCAAACTCCAGTAGAAGGTGCCCAGACTTCCATTTATTT  
GGCCTCTTCACCTGAGGTAGAAGGAGTGTGAGGAAGATACTTTGGGGATTGTAAAGAGGAAG  
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTCTGGGATATCAGTGAAGTG  
ATGGTTGGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAACTGCATATCAG  
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACTTGAAGAAAAGAATTTTG  
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTT  
TGGGATAAGAGAATTTAGCAAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA  
GTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCAAGCATGGATGACATATTA  
ATATTTGTCAGAATTAAGTGAAGTCAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT  
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTGTTGTGTGGAAATTATCTGC  
CTGGTGTGTGCACACAAGTCTTACTTGGAATAAATTTACTGGTAC

## FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE  
LLRLGARVIMGCRDRARAEAAAGQLRREL RQA AECGPEPGVSGVGELIVRELDLASLRSVRA  
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNHLGHFLLTNLLLGLLKSSAPSR  
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSLANILFTRELARRLEGTVNVTNVNLHPG  
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE  
LLPKAMDESVARKLWDISEVMVGLLK

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Short-chain alcohol dehydrogenase family protein**

amino acids 134-144, 44-56 and 239-248

#### **N-glycosylation site.**

amino acids 212-215 and 239-242

09978299-101501  
TOSTOT " 662660

## FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN  
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAAATAGGAACAAGGAGTAAAAGAGCTGTT  
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT  
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG  
TTACTGAAAAATTATTTTTGGGATAAGAGAATTCAGCAAAGATGTTTTAAATATATATAGT  
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCA  
AGCATGGATGACATATTAATATTTGTCAGAATTAAGTGAAGTCAAAGTGCTATCGAGAGGTTT  
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT  
TGTGTGGAAATTATCTGCCTGGCTT

09978299-101501  
F05T0T" 6628/660



## FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGGAGCCCAGCC  
CTTTCCCTAACCCAACCCAACCTAGCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGAC  
CCCAGCGTTACCAATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCT  
GCTCCTGGTAACTTGGGTTTTTTACTCCTGTAACTGAAATAACAAGTCTTGCTACAGAGA  
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGT  
CGTTTCAGTCAGATGTTGCATCCAATTTTGGAGGAAGCTTCCGATGTCATTAAGGAAGAATT  
TCCAAATGAAAATCAAGTAGTGTGTCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC  
AGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAG  
AGAGAATACAGGGGTGAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAG  
TGACCCCATTCAGAAATTCGGGACTTAGCAGAAATCACCACTCTTGATCGCAGCAAAAGAA  
ATATCATTGGATATTTTGGAGCAAAAGGACTCGGACAACTATAGAGTTTTTGAACGAGTAGCG  
AATATTTTGCATGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAACCCGAAAG  
ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACT  
TGGGAGCTATGACAAATTTTGGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTT  
GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT  
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCCAGAATGAAGTAGCTCGGC  
AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT  
CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGTCTGTAATCGCTATTGACAGCTTTAG  
GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCCTGGAAAACCTCAAGCAATTG  
TATTTGACTTACATTCTGGAAAACCTGCACAGAGAATTCCATCATGGACCTGACCCAACTGAT  
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA  
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTTAAAAACTTG  
AAAAACAGTTTGTAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAATAGTAAACCTA  
TATTTTCATAATTCTATGTGTATTTTTATTTTGAATAAACAGAAAGAAATTTAAAAA  
AAAAA

09978299 "10501

[illegible]

&lt;subunit 1 of 1, 406 aa, 1 stop

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNADVALVNFYADWCRFSQ  
MLHPIFEEASDVIKEEFPNENQVVFARVDCDQHSDIAQRYRISKYPTLKLFRNGMMMKREYR  
GQRSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKDSDNRYRVFERVANILH  
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDTVYNWIQDKCVPLVREI  
TFENGEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH  
IQKTPADCPVIAIDSFRHMYVFGDFKDVLIPGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG  
EOAODVASSPPESSFQKLAPSEYRYTLLRDRDEL

**Signal peptide:**

amino acids 1-29

amino acids 403-406

## amino acids 203-211

## amino acids 50-66

## FIGURE 126

ATTAAGGAAGAATTTCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA  
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATG  
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

09978299-101501  
T05T0T" 156282660

## FIGURE 127

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTGCGCCGCNNGAGCCCGGGTCGAGAGGACNAGG  
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCCCTTTCCTAACCC  
AACCCAACCTAGCCCNGTCCCAGCCGCCAGCGCCTGTCCCTGTCNCGGANCCCAGCGTNACC  
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC  
TTGGGTTTTTACTCCTGTAACAACTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA  
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTGCTTTTCAGTCAG  
ATGTGGCATCCAATTTTTGAGGANGCTTCCGATGTCATTAAGGAAGAATTTCCAAATGAAAA  
TCAAGTAGTGTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA  
TAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG  
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

09978299.101501

## FIGURE 128

GCCCACGCGTCCGATGGCGTTACGTTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA  
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTGATGAGCTGAAGACTGAT  
TACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGTA  
CTCCCAGAGTACCTCAT  
CCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA  
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGA  
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATG  
GTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTT  
TGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGAAAAAGCCAC  
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT  
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTTGCTTGTGGAAAGACTG  
TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT  
GATTACCTCTGGTGTGACAGGTTTGAACCTTGCACTTCTTAAGGAACAGCCATAATCCTCTG  
AATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTTTATAGGAACTTGTA  
GGGCTCATTTTGGTTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC  
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCTCATCTGTC  
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTT  
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA.  
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT  
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAG  
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG  
TACTACAGATTTTCAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCCTTAGT  
GCAATACAATAAACTCTGAAATTAAGACTC

09978299 "101501

## FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF  
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLA  
FYLLAFFYYLYGMIYVLVSS

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Type II transmembrane domain:**

amino acids 11-31

#### **Other transmembrane domain:**

amino acids 57-77 and 123-143

09978299-101501  
TOSTOT-66284660

## FIGURE 130

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCTG  
AATCCCCTTGTA TACTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC  
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCTCTTGGCATATCATATTTGGAGGTATA  
TGAGTAGACCAGTGATGAGTGGCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT  
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTT  
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATT  
GGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT  
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

0978299-101501  
FOSTOT" 65284660

## FIGURE 131

CGGACGCGTG GGGGAAACCTTCCGAGAAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG  
GAACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAAGCTGGGGCTCCCGCCGC  
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTCCGGGACCGCTTCGGCTGAAGCATTTGAC  
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACAC  
CTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTC  
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA  
GAAGCATATTCCTAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC  
ATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC  
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC  
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCC  
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA  
GCAAAATGTCCTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGA  
GAAAGTGATGGCTTTTAAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACCTCT  
TGTCCTCTCGGTGATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGC  
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG  
CTAAACAGATATCCAGCTTCTTCTCTTGTGGTTGTTAGATCTAAACTGAAGATCATGAAGA  
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTT  
AAAAGACAAGTGTAATAGACATCTAAAATTCACCTCCTCATAGAGCTTTTAAATGGTTTCA  
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

0978299-101501  
TOSTOT 65284550



## FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGS LWVRTQLGLPPLLLLT MALAGGSGTASAEAFDSVLGDTASCHRAQLTYPLHTYP  
KEEELYACQRCRLFSICQFVDDGIDLNRKLECE SACTEAYSQSDEQYACHLGCQNQLPFA  
ELRQEQLMSLMPKMHL LFP LTLVRSFWSDMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEI  
QYAPHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVL  
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG  
PLPTKVNLAHSEI

### **Important features:**

#### **Signal peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 241-260

#### **N-glycosylation site.**

amino acids 90-93

09978299.101501  
TOSTOT"66282660

## FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACACCTACCC  
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG  
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA  
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTTCGC  
TGAAGTGAAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAA  
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

09978299 . 101501

## FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA  
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC  
CCAACCTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGCCCGGAGGTTGCGGGACCG  
CTTCGGCTGAAGCATTTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG  
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG  
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG  
AATGTGAATCTGCATGTACAGAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTT  
GGTTGCCAGAATCAGCTGCCATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC  
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT  
CCGC

09978299-101501  
TOSTOT" 6628/660

## FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCGGAGGT  
GGGGCGCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCGACCGAGC  
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGCCGCGGCTG  
GGGATTCTTGTTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC  
AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT  
ACCTGTGATGTTGAAACCATTGATAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAAA  
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCCTTTCT  
GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA  
GTTCTTGATGGAATTAAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA  
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA  
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC  
ATTGAGTCCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA  
CAAGGGACCAGATGCTTGGAAAATATGGAATGTCATCTACGAAGAAAAGTGTTTTAAGCCAC  
AGACAATTAAAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACACT  
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGG  
CCTACATGCAAGCATTAAATGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAG  
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGACTGAA  
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTT  
ATCCAAAGTGTTACCATTCTTCGAGCGCCCAGATTTTCAACTCTTTACTGGAAATAAAATTC  
AGGATGAGGAAAACAAAATGTTACTTCTGGAAATACTTCATGAAATCAAGTCATTTCTTTG  
CATTTTGATGAGAATTCATTTTTTGCTGGGGATAAAAAAGAAGCACACAACTAAAGGAGGA  
CTTTGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC  
GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG  
AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATTCCATCTAACCAGACAAGA  
AATAGTATCATTATTCAACGCATTTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAAGT  
TCAGGAACTTGTTACAGAATATTCATTAAAGAAAACAAGCTGATATGTGCCTGTTTCTGGAC  
AATGGAGGCGAAAGAGTGAATTTTCAATCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA  
ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTTAAGTAAACACATTTT  
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAAGTAATACTTTAATAATGTG  
GTACAAATTTTAAAGTTTAAATATTGAATAAAAGGAGGATTATCAAATTAATAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

0978299.101501

## **FIGURE 136**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974

<subunit 1 of 1, 468 aa, 1 stop

<MW: 54393, pI: 5.63, NX(S/T): 2

MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAAQRCFCQVSGYLDDCTCDVETIDRFNNYRLF  
PRLQKLLESDFRYKVNLRPCPFWNDISQCGRDCAVKPCQSDEVPDGIKSASYKYSEEA  
NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNP  
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAF  
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI  
ELRALSKVLPFFERPDFQLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH  
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTQGLGTALKILFSEKLIANMPESGPSYEFH  
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **N-glycosylation site.**

amino acids 280-283 and 384-387

#### **Amidation site.**

amino acids 94-97

#### **Glycosaminoglycan attachment site.**

amino acids 20-23 and 223-226

#### **Aminotransferases class-V pyridoxal-phosphate**

amino acids 216-222

#### **Interleukin-7 proteins**

amino acids 338-343

09978299.101501  
T05T01"66282660

## FIGURE 137

GCTGGAAATATGGATGTCATCTACGAGAACTGTTTTAAGCCACAGACAATTAAAAGACCTT  
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA  
GGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA  
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA  
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGAAGGAGAAGGTCCAAGAAGG  
CTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCAT  
CTTNGAGCGCCCAGATTTTCAACTNTTTACTGGAAATAAAATTCAGGATGAGGNAAACAAAA  
TGTTACTTTTGGAAATACTTCATGAAATCAAGTCATTTCTTTGCATTTTGATGAGAATTCA  
TTTTTTTGCTG

09978299-101501  
TOSTOT 55282660

## FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGGCAGGATGGGAGGGAA  
AGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC  
CGATCAGGCATGGAACTCCCCTTCGTCACTCACCTGTTCTTGCCCCCTGGTGTTCTTGACAGG  
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTCCCAGGGCCACCAGAAG  
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC  
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG  
GGCCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTC  
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTC  
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA  
GTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGTCAAGGAGTTAAAAACCCTAGAAAGCAAA  
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT  
GCCCTCCCAAGCCTGGGAGTAACTATTTCCCCCATCCCAGGCCTGTGCCCTCTCTGGTCT  
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCCGTGTGGATGCTTCATTCCA  
GCCTCAGGGAAGCCTGGCACCCACTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT  
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCTGGCAAAGGG  
CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAGCTCCATGTTTCCTAACAGA  
TTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG  
GTGGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT  
CTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA  
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG  
AGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA  
AATAATAATAATAATAATTACAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA  
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG  
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

## **FIGURE 139**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039

><subunit 1 of 1, 124 aa, 1 stop

><MW: 13352, pI: 5.99, NX(S/T): 1

MELPFVTHLFLPLVFLTGLCSPFNLDHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW

DGPSGDRRGDVYRCPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **Cell attachment sequence.**

amino acids 70-73

#### **N-glycosylation site.**

amino acids 98-101

#### **Integrins alpha chain proteins**

amino acids 67-81

09978293-101501  
TOSTOT" 66284660



## FIGURE 140

CACAGTTCCCCACCATCACTCNTCCCATTCCCTTCCAACTTTATTTTTAGCTTGCCATTGGGA  
GGGGGCAGGATGGGAGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC  
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACTCCCCTTCGTCACTCACCTGTTCTTG  
CCCCTGGTGTTCCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT  
ATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC  
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT  
TATCGCTGCCCTGTAGGGGGGGCCCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA  
CCAAGTGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA  
CAGATGGTGATGG

0998299.101501  
TDSFOT" 65284660

## FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCGGGCTCTAGAACA  
ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA  
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT  
ACGCATTGATTCCATGTTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCCCTCAGAACCTC  
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCCTGGAGA  
AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
GGATCCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTTGAGTGTGATGTCACTGATGACATC  
ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG  
GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC  
CTTGTTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG  
GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA  
CATTCTGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCTTTGTTGGCTTCATGCTGATCCTTGT  
GGTCTGTGCCACTGTTCTGTCTGGAATAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG  
TGGTCTCCCGAGACACCTTGAAAATAACCAATTCACCCAGAAAGTTAATCAGCTGCAGAAAG  
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGAT  
CTCATAGGTTTTCGGAAGGGCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC  
ATGAGGGGACAAGTTGTGTTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC  
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC  
CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC  
TACACACCTGCTAAACACACACACACAGAGTCTCTCTATATATACACACGTACACATAAA  
TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTCAG  
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT  
GGCTTGGAGAGCCCACTTTCCCAAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
TGTTGAGTTCACTTCAAGCCCAATGCCGGTGACAGGGGAATGGCTTAGCGAGCTCTACAGT  
AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC  
CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT  
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTTC  
TGTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA  
AAAAAAAAA

09973299 " 101501

## **FIGURE 142**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPGE  
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTS  
SILKHPFNRNSTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG  
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPVLALFAFVGFMLILV  
VVPLFVWKMGRLLQYSCCPVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

### **Important features:**

#### **Signal peptide:**

amino acids 1-29

#### **Transmembrane domain:**

amino acids 230-255

#### **N-glycosylation site.**

amino acids 40-43 and 134-137

#### **Tissue factor proteins.**

amino acids 92-119

#### **Integrins alpha chain proteins**

amino acids 232-262

09978899.101501

## FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACAATTGAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG  
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG  
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCTAGGGCCACATTGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG  
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC  
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

097829-10501

## FIGURE 144

CCCACGCGTCCGCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA  
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA  
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG  
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC  
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA  
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGG  
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG  
GCTGCTTTGGCATTGTTGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT  
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGCAGGGCGTTGGG  
CAGGGGTCCCTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCTCGAGC  
GCTGGTACTCTGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG  
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGC  
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA  
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCCATTAAAGGCTCAGCACTGGAGGAGAGA  
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCT  
GTGGTCAATGTGTCTGGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGCGGCTGCT  
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTG  
AGGTGCAGCTCATTCACCTTCAACCAGGAAGTCTACGGGAATTTACGCGCTGCCTCCCGCGGC  
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCATTCTCT  
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTC  
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC  
TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTACCTGGATCCTCATTGACCGGGCCCTCAA  
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT  
TCCAGAGCCTCAGCGGTAACAGCCGGCCCTGCAGCCCTTGGCCCACAGGGCACTGAGGGGC  
AACAGGGACCCCGGCACCCCGAGAGGCGCTGCCGAGGCCCAACTACCGCCTGCATGTGGA  
TGGTGTCCCCCATGGTCGCTGAGACTCCCCTTCGAGGATTGCACCCGCCCCGTCTAAGCCTC  
CCCACAAGGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTA

## FIGURE 145

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC  
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPL  
LYSHRLSELRLFLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL  
FVNVASTSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE  
TVTWILIDRALNITSLQMHSLRLLSQNPSPQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER  
RCRGPNYRLHVDGVPHGR

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 177-199

#### **N-glycosylation site.**

amino acids 118-121, 170-173 and 260-263

#### **Eukaryotic-type carbonic anhydrases proteins**

amino acids 222-270, 128-164 and 45-92

09978299.101501  
F05101"66282660

# FIGURE 146

GGCGCCTGGTTCCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCCGCCAGCCTCCGCCGCCGAGCCTC  
 GTTCGTGTCCCCGCCCCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGGGGCGCCCCACCCTGGCAGACTAACGAA  
 GCAGCTCCCTTCCCACCCCAACTGCAGGTCTAATTTTGGACGCTTTGCCTGCCATTTCTTCCAGGTTGAGGGAGC  
 CGCAGAGGCGGAGGCTCGCGTATTCTTGCAGTCAGCACCCACGTGCGCCCCGGACGCTCGGTGCTCAGGCCCTTC  
 GCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGGCCGTCCGGTTTGGCT  
 CACCTCTCCAGGAACTTCACTGAGAGCCAAAGAGGTGGAAGAGCCTGTCTTGGAGATTTTCTGGGGAA  
 ATCCTGAGGTCAATTCATTATGAAGTGTACCGCGCGGAGTGGCTCAGAGTAACCACAGTGCTGTTTCATGGCTAGA  
 GCAATTCAGCCATGGTGGTCCCAATGCCACTTTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT  
 GAGTGGTGGATAGCCAAACAACGAGGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCAT  
 AATAAATTACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA  
 TCTGCAGAACTCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGCTTCCATCAATTGGACAGAAT  
 TTGGGAGCACACTGGGGAAGATATAGGCCCCCGACGTTTTCATGTACAATCGTGGTATGATGAAGTGAAAGACTTT  
 AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTAGGTGTTCTGGCCCTGTATGTACACATTATACA  
 CAGGTCTGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAATTTGTGTCTATAACATGAACATCTGGGGGCAG  
 ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAAGGGAACTGGTGGGGCCATGCCCTTACAAA  
 CATGGGCGGCCCTGTTCTGCTTGCCACCTAGTTTTGGAGGGGGCTGTAGAGAAAATCTGTGCTACAAAGAAGGG  
 TCAGACAGGTATATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAGTCACAAGTCCATGACACC  
 CATGTCCGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCGCACAGCAAATGTCCCAAATGTTTCT  
 TGTGAAGTAAGATTAAGAGATCAGTGCAAAGGAACAACCTGCAATAGGTACGAATGTCTGCTGGCTGTTTGGAT  
 AGTAAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT  
 ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTTATTTTCATCAAGTCCAATAGA  
 AATGGTATTCAAACAATTGGCAAATATCAGTCTGCTAATTCCTTACAGTCTCTAAAGTAACAGTTCAGGCTGTG  
 ACTTGTGAAACAACCTGTGGAACAGCTCTGTCCATTTTATAAGCCTGCTTCACATTGCCCAAGAGTATACTGTCT  
 CGTAACTGTATGCAAGCAAATCCACATTATGCTCGTGTAAATTGGAACCTGAGTTTATTTCTGATCTGTCCAGTATC  
 TGCAGAGCAGCAGTACATGCTGGAGTGGTTGCAAAATCACGGTGGTTATGTTGATGTAATGCCTGTGGACAAAAGA  
 AAGACCTACATTGCTTCTTTTTCAGAATGGAATCTTCTCAGAAAGTTTACAGAATCCTCCAGGAGGAAAGGCATT  
 AGAGTGTGTTGCTGTTGTGTGAAGTGAATACTTGAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA  
 ATTTTGTATAAACTGTAACTACTGTACAGAGTACATCAACTATTTTCAGCCCAAAAAGGTGCCAAATGCATA  
 TAAATCTTGATAAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATATAATGG  
 TTTTAGAAATCCTGTGTTAAATATTGCTATATTTTCTTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT  
 GTTCTACGTTTTCATATATTATATGGTGCTTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG  
 GCCCTCAGAAAATCATCTAGTGCATTTAAAAATAATCGACTCTAAACTGAAAGAAACCTTATCACATTTTCCCC  
 AGTTCAATGCTATGCCATTACCAACTCCAAATAATCTCAATAATTTTCCACTTAATAACTGTAAAGTTTTTTTTC  
 TGTTAATTTAGGCATATAGAATATTAAATCTGATATTGCACTTCTTATTTTATATAAAATAATCCTTTAATATC  
 CAAATGAATCTGTTAAATGTTTGATTCTTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGGT  
 ATGAAAACATTCTTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTTCTATGTACTGTTA  
 AAATTGAGGTACATATTTTCTTTTGTATCCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTT  
 GAACAAAGATGAACTAATGTATTACATTACCATTGCCACTGATTTTTTTTAAATGGTAAATGACCTTGTATATAA  
 ATATTGCCATATCATGGTACCTATAATGGTGATATATTTGTTTCTATGAAAAATGTATTGTGCTTTTGATACTAAA  
 AATCTGTAAATGTTAGTTTTTGGTAATTTTTTTTCTGCTGGTGGATTACATATTAAATTTTTTCTGCTGGTGGAA  
 TAAACATTAAATTAATCATGTTTCAAAAAAAAAAAAAA

09978299 101504

## **FIGURE 147**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAI PAMVVPNATLLEKLLEKYMDEEDGEWWIAKQRGKRAITDNDM  
QSILDLHNKLR SQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW  
GRYRPPTFHVQSWYDEVKDFSYPYEHECNFYCPFRCSGPVCTHYTQV V WATSNRIGCAINLC  
HNMNIWGQIWPKAVYLV CNYSPKGNWWGHAPYKHGRPCSACPPSFGGGCRENL CYKEGSDRY  
YPPREEETNEIERQQSQVHDTHVRTRSDSSRNEVIS AQQMSQIVSCEVRLRDQCKGTT CNR  
YEC PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKH YFIKSNRNGI  
QTIGKYQSANSFTVSKVTVQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG  
TRVYSDLSSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPGGKA FRV  
FAVV

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein**

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

#### **N-glycosylation site**

amino acids 28-31

0978299.101501  
TOSTOT" 66284660



## FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG  
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT  
GGCGTCTCCGGGCCCGCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCG  
CGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGT  
ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC  
AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT  
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAAGCTGC  
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGAA  
GAATAGGGTGAAAAACCTCAGAAGGGGAAAACTCCAAACCAGTTGGGAGACTTGTGCAAAGGA  
CTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCCTTTC  
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAG  
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCAGATGGGAGACCCATCTCTCTTGTGCT  
CCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTTAA  
AAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGA  
GGAACAATGAGCTTGGTGGACACATTTCAATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGC  
TTCCGCTTAGAGGTCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG  
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT  
CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCT  
GGTTAATTTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC  
CTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA  
TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAAC  
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA  
AACCTTCAAAGCATGTTTCTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT  
TTGTGATTCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTTCGAAAGCTAAGAT  
GACCATGCGCCCTTTCCTCTGTACATATAACCCTTAAGAACGCCCCCTCCACACACTGCCCC  
CAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCAT  
TGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAA  
AAAAAAAAAA

09978259 101501

## FIGURE 149

MSLLPRRAPPVSMRLAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH  
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

Signal sequence:

amino acids 1-34

09978299.101501

# FIGURE 150

GCCCCAGGGACTGCTATGGCTTCCTTTGTTGTTACCCCCGGTCTGCGTCATGTTAAACTCCAATGTCTCTCTGTG  
 GTTAACTGCTCTTGCCATCAAGTTCACCTCATTGACAGCCAAGCACAGTATCCAGTTGTCAACACAAATTATGG  
 CAAAATCCGGGGCCCTAAGAACACCGTTACCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCCTA  
 TGCCTCACCCCCCACTGGAGAGAGGGCGGTTTTAGCCCCCAGAACCCCCGTCTCTGGACTGGCATCCGAAATAC  
 TACTCAGTTTGCTGCTGTGTGCCCCCAGCACCTGGATGAGAGATCCTTACTGCATGACATGCTGCCCATCTGGTT  
 TACCGCCAATTTGGATACTTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCCCTTTACTTAAACATCTACGT  
 GCCCACGGAAGATGGAGCCAACACAAAGAAAAACGCAGATGATATAACGAGTAATGACCGTGGTGAAGACGAAGA  
 TATTCATGATCAGAACAGTAAGAAGCCCGTCATGGTCTATATCCATGGGGGATCTTACATGGAGGGCACCGGCAA  
 CATGATTGACGGCAGCATTTTGGCAAGCTACGGAAACGTCATCGTGATCACCAATTAACCTACCGTCTGGGAATACT  
 AGGGTTTTTAAGTACCGGTGACCAGGCAGCAAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCACTGCGGTG  
 GATTGAGGAGAATGTGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGGCTGGGGCCTC  
 CTGTGTGACGCTGTTGACCCTGTCCCACTACTCAGAAGGTCTCTTCCAGAAGGCCATCATTACAGAGCGGCACCGC  
 CCTGTCCAGCTGGGCAGTGAACCTACCAGCCGGCCAAGTACACTCGGATATTGGCAGACAAGGTGCGCTGCAACAT  
 GCTGGACACCACGGACATGGTAGAATGCCTGCGGAACAAGAATACAAGGAGCTCATCCAGCAGACCATCACCCC  
 GGCCACCTACCACATAGCCTTCGGGCGGGTGATCGACGGCGACGTCTCCAGACGACCCCCAGATCCTGATGGA  
 GCAAGGCGAGTTCTCAACTACGACATCATGCTGGGCGTCAACCAAGGGGAAGGCCCTGAAGTTCTGACGGCAT  
 CGTGGATAACGAGGACGGTGTGACGCCCAACGACTTTGACTTCTCCGTGTCCAACCTTCGTGGACAACCTTTACGG  
 CTACCCTGAAGGGAAAGACACTTTGCGGGAGACTATCAAGTTTATGTACACAGACTGGGCCGATAAGGAAAACCC  
 GGAGACGCGCGGGAACCCCTGGTGGCTCTCTTTACTGACCACAGTGGGTGGCCCCCGCGTGGCCGCGGACCT  
 GCACGCGCAGTACGGCTCCCCACCTACTTCTATGCCTTCTATCATCACTGCCAAAGCGAAATGAAGCCAGCTG  
 GGCAGATTGCGCCCATGGTGTAGGTTCCCTATGTCTTCGGCATCCCCATGATCGGTCCCAACCGAGCTCTTCAG  
 TTGTAACTTTTCCAAGAACGACGTATGCTCAGCGCCGTGGTTCATGACCTACTGGACGAACCTTCGCCAAAACCTGG  
 TGATCCAAATCAACCAGTTCTCAGGATACCAAGTTTATTACACAAAACCCAAACCGCTTTGAAGAAGTGGCCTG  
 GTCCAAGTATAATCCCAAAGACAGCTCTATCTGCATATTGGCTTGAAACCCAGAGTGAGAGATCACTACCGGGC  
 AACGAAAGTGGCTTTCTGGTTGGAACCTCGTTCCTATTTGCACAACCTTGAACGAGATATTCCAGTATGTTTCAAC  
 AACCACAAAGGTTCTCCACAGACATGACATCATTTCCCTATGGCACCCCGCGATCTCCCGCCAAGATATGGCC  
 AACCACAAACGCCCAGCAATCACTCCTGCCAACAATCCCAAACACTCTAAGGACCCCTCACAAAACAGGGCCTGA  
 GGACACAACCTGTCCTCATTGAAACCAAACGAGATTATCCACCGAATTAAGTGTACCATTGCCGTGCGGGCGTC  
 GTCCTCTTCTCAACATCTTAGCTTTTGCGGCGCTGTACTACAAAAGGACAAGAGGCGCCATGAGACTCACAG  
 GCGCCCCAGTCCCCAGAGAAAACACCAAAATGATATCGCTCACATCCAGAACGAAGAGATCATGTCTCTGCAGAT  
 GAAGCAGCTGGAACAGATCACGAGTGTGAGTCGCTGCAGGCACACGACACACTGAGGCTCACCTGCCCGCCAGA  
 CTACACCTCACGCTGCGCCGGTCGCCAGATGACATCCCACTTATGACGCCAAACACCATCACCATGATTCCAAA  
 CACACTGACGGGGATGCAGCCTTTGCACACTTTTAAACACCTTCAGTGGAGGACAAAACAGTACAAATTTACCCCA  
 CGGACATTCCACCACTAGAGTATAGCTTTTGCCCTATTTCCCTTCTATCCCTCTGCCCTACCCGCTCAGCAACAT  
 AGAAGAGGGAAGGAAAGAGAGAAGGAAAGAGAGAGAGAAAGAAAGTCTCCAGACCAGGAATGTTTTGTCCCACT  
 GACTTAAGACAAAAATGCAAAAAGGCAGTCATCCATCCCGGCAGACCCTTATCGTTGGTGTTTCCAGTATTAC  
 AAGATCAACTTCTGACCCTGTGAAATGTGAGAAGTACACATTTCTGTTAAAATAACTGCTTTAAGATCTCTACCA  
 CTCCAATCAATGTTTAGTGTGATAGGACATCACCATTTCAAGGCCCGGGTGTTCCAACGTCATGGAAGCAGCT  
 GACACTTCTGAAACTCAGCCAAGGACACTTGATATTTTTTAATTACAATGGAAGTTTAAACATTTCTTTCTGTGC  
 CACACAATGGATGGCTCTCCTTAAGTGAAGAAAGAGTCAATGAGATTTTGCCCAGCACATGGAGCTGTAATCCAG  
 AGAGAAGGAAACGTAGAAATTTATTATTAAGAATGGACTGTGCAGCGAAATCTGTACGGTTCTGTGCAAGAG  
 GTGTTTTGCCAGCCTGAACATATTTAAGAGACTTTGT

## **FIGURE 151**

MLNSNVLLWLTALAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP  
PTGERRFQPPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMLPIWFTANLDTLMTYVQDQN  
EDCLYLNIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI  
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR  
VTIFGSGAGASCVSLTLTSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCNML  
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLGV  
NQGEGLKFVDGIVDNEDGVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIKFMYTDWADKENP  
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKP SWADSAHGDEVYV  
FGIPMIGPTELFSCNFSKNDVMLS AVVMTYWTNFAKTGDPNQVPVQDTKFIHTKPNRFEEVA  
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPDMTS  
FPYGTRRSPAKIWPTTKRPAITPANNPKH SKDPHKTGPEDTTVLIETKR DYSTELSVTI AVG  
ASLLFLNILAFAALYYKKDKRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE  
SLQAHDTLRLTCPPDYTLTLRRSPDDIPLMTPNTITMI PNTLTGMQPLHTFNTFSGGQNSTN  
LPHGHSTTRV

### **Signal sequence:**

amino acids 1-24

### **Transmembrane domains:**

amino acids 189-204, 675-692

# FIGURE 152

GGGAAAGATGCGGGCGACTCTGGGACCCCTTGGGTCTGGCAGCAGTGGCGGCGATGTTTGT  
 CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTTCTTTTGTGGGGTCTGGGCAGGGGCCA  
 CAGCAAGTCGGGGCGGGTCAAACGTTTCGAGTACTTGAAACGGGAGCACTCGCTGTCTGAAGCC  
 CTACCAGGGTGTGGGCACAGGCAGTTCCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA  
 TGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCTTGTGGAACCGG  
 GTGCCATGTTTCTTGAGAGACTGGGAGTTGCAGGTGCACTTCAAAATCCATGGACAAGGAAA  
 GAAGAATCTGTCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC  
 CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT  
 GAGGAGAAGCAGCAAGAGCGGGTATTCCCCTACATCTCAGCCATGGTGAACAACGGCTCCCT  
 CAGCTATGATCATGAGCGGGATGGGCGGCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC  
 GCAATCTTCATTACGACACCTTCCCTGGTGATTCTGCTACGTCAAGAGGCATTTGACGATAATG  
 ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCCGGAGTCCGCCTGCC  
 CCGCGGCTACTACTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA  
 TTTCTTGAAGTTGTTTGAACCTGACAGTGGAGAGAACCCAGAAAGAGGAAAAGCTCCATCGA  
 GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC  
 CCTGAGTGGCCTGGCCCTCTTCCCTCATCGTCTTTTCTCCCTGGTGTCTTCTGTATTTGCCA  
 TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA  
 GCCCTCCTGCTGCCACCACTTTTGTGACTGTCAACCATGAGGTATGGAAGGAGCAGGCACTG  
 GCCTGAGCATGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTG  
 TCACTGGAGTTTGAATGCAGGGACCCCGCATTTCCCATGGTTGTGCATGGGGACATCTAACT  
 CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCTTTCCCTGCAGTCC  
 TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAAATCACAGAAC  
 AGAATTTCATAGCCAGGCTGCCGTGTTGTTGACTCAGAAGGCCCTTCTACTTCAGTTTTG  
 AATCCACAAAGAATTAAAACTGGTAACACCACAGGCTTTCTGACCATCCATTCTGTTGGGTT  
 TTGCATTTGACCCAACCCTCTGCCTACCTGAGGAGCTTTCTTTGGAAACCAGGATGGAACT  
 TCTTCCCTGCCTTACCTTCTTTCACTCCATTCAATTGTCCTCTCTGTGTGCAACCTGAGCTG  
 GGAAAGGCATTTGGATGCCTCTCTGTTGGGGCCTGGGGCTGCAGAACACACCTGCGTTTCAC  
 TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTGTTCCCTAGCAT  
 GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG  
 AAGTTTGGCTAAAGGTTGGTGTAATAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG  
 GATTAGCTGTGCAACTGACCAGCTCCAGGTTTGATCAAACCAAAGCAACATTTGTTCATGTG  
 GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTTGTAGT  
 TACGATTTTTGGAATCCCACTTTGAGTGCTGAAAGTGTAAGGAAGCTTTCTTCTTACACCTT  
 GGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTTTCTTAATGGACAAGAGACAGT  
 TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCTGGAAGAGTT  
 CACTGTCAATTGAGCAGCACAGCCTGAGTGCTGGCCTCTGTCAACCCTTATTCCACTGCCTTA  
 TTTGACAAGGGGTTACATGCTGCTCACCTTACTGCCCTGGGATTAAATCAGTTACAGGCCAG  
 AGTCTCCTTGGAGGGCCTGGAACCTCTGAGTCCTCCTATGAACCTCTGTAGCCTAAATGAAAT  
 TCTTAAATCACCGATGGAACCAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCG  
 ACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

09975299-101501

## FIGURE 153

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911

><subunit 1 of 1, 348 aa, 1 stop

><MW: 39711, pI: 8.70, NX(S/T): 1

MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPQQVGAGQTFEYLKREHSLSKPYQ  
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQ GALWNRVPCFLRDWELQVHF KIHGQGKKN  
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVD TYPNEEKQQERVFPYISAMVNNGSLSY  
DHERDGRPTELGGCTAIVRNLHYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG  
YYFGTSSITGDLSDNHDVISLKL FELTVERTPEEEKLHRDVFLPSVDNMKLPMTAPLPPLS  
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

### Signal sequence:

amino acids 1-38

### Transmembrane domain:

amino acids 310-329

09978299.101504  
TOSTOT 6628660

# **FIGURE 154**

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT  
 CTGATGGTGGGTGCTTAACTCAGTGGGACTCCAAGATTTCCATGAAGAAAATCAGTTGTCTTCATTCAAGAAT  
 TGGGGTCTGGCTCAGAATTCTTGCAGCTGGTGAAAATCTGTTTTCTAGAAGAGGTTTAAATTAATGCCTGCAGTCT  
 GACATGTTCCCGATTTGAGGTGAAACCATGAAGAGAAAATAGAATACTTAATAATGCTTTTTCCGCAACCGCTTCT  
 TGCTGCTGCTGGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATCCCGGTGT  
 CGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCCGACCCCTGTGACGGAGCCCCCTGTGA  
 CAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGTGGCCGAGCGCAGCATGGAAGGTCATGCC  
 CGCATCATTTTAAGCTGGTCTCAGTGCATGTGTTCAATTCGCCACGGAGACAGGTACCCACTGTATGTCATTCCTCA  
 AAACAAAGCGACCCAGAAATTGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAACCTGGAAGCTTTCA  
 TTAGTTCACATGTCAAAGGATCCGGAGCCTCTTTGAAAGCCCCTTGAACCTCCTTGCCTCTTTACCCAAATCACC  
 CATTTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTCAGAACGGTCAGCTGCTGAGGGATA  
 TCTATCTAAAGAAACACAAACTCCTGCCCAATGATTGGTCTGCAGACCAGCTCTATTTAGAGACCCTGGGAAAA  
 GCCGGACCCCTACAAAGTGGGCTGGCCTTGCTTTATGGCTTTCTCCAGATTTTGAAGTGAAGAAATTTATTTCA  
 GGCACCAGCCAAGTGCGCTGTTCTGCTCTGGAAGCTGCTATTGCCCGGTAAGAAAACCATGATCTGGAAAAGGAGC  
 AGCGTCGTCAGTACCTCCTACGTTTGA AAAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCAAGATCGTGG  
 ATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCACAATGTCAGCT  
 TTCCCTGTACCAGAAATGGCTGTGTTGACATGGAGCACTTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA  
 GGGAAAGACGGGAGAAGAAATTGTAATTCGGGTATTCTCTCCTGGGTGCCACCCCATCTGAACCAAACCATCG  
 GCCGATGCAGCGTGCCACCGAGGGCAGGAAAGAAGAGCTCTTGGCCCTCTACTCTGCTCATGATGTCACCTGT  
 CACCAGTTTCTCAGTGCCTTGGGCCTTTGAGAAGCCAGGTTCCCAAGGTTTGCAGCCAGGTTGATCTTTGAGCTTT  
 GGCAAGACAGAGAAAAGCCAGTGAACATTCCGTCCGATTCTTTACAATGGCGTCGATGTCACATTCCACACCT  
 CTTTCTGCCAAGACCACCACAAGCGTTCTCCAAGCCCATGTGCCCGCTTGAAAACCTGGTCCGCTTTGTGAAA  
 GGGACATGTTTGTAGCCCTGGGTGGCAGTGGTACAAATTATTATGATGCATGTCACAGGGAAGGATTTCTAAAGG  
 TATGCAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAGGTCCACTTCTAGTTTTGTCTGTTAC  
 TAAGGGTAGAAGATTATTGCTTTTTTAAAGGCTAAATATTGTTTGTGGGAACCAAGATGGTTGGGGTTGAACAGT  
 AAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGGCCAGTTCACAGAGGAATAGAAGGTACTT  
 TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC  
 TCTTCTGGCCTGCCCCATGTTACTATGTGATGGAACCAGCACACCTCAACCAAAATTTTTTAAATCTTAGACATT  
 TTTACCTTGTCTTGTGAAGATTTCTTGAAGTGATTTATCTAAAATAAAGGTTGGCAAACCTTTTTCTGTAAAGG  
 GCCAGATTGTAAATATTTTCAAGTGTGTGGACCAAAAGGCCACATACAGTCTCTGTCTAACTACTCAACTCTGT  
 TTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAAGGAATATGTGTAGCTGGGTTCCAGGCCAGACAAAACA  
 GATGGTGACCAGACTTGGCCCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAAAATAGGCTATACATAAATTGC  
 ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAATTATTCAATGGTTCCTCCAGTAACTTCTGCTAGAAACA  
 CAGAATTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAA  
 AACTGATTAGAAGAATACTTGATGTTTATGATGATTGTGGTACAAGATAGTTTTAAGTATGTTCTAAATATTTGT  
 CTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTTGTATGCCATTTAGTATTTTTATAGTTTAGGAAAATATT  
 TTCTAAGACCAGTTTTAGATGACTCTTATTCCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAG  
 GAGGCTAGAAGATGAATTCAGGCACTTTCTTCCAATAAACTAATTATGGCTCATTCCCTTTGACAAGCTGTAGA  
 ACTGGATTCATTTTTAAACCATTTTCATCAGTTTCAAATGGTAAATTTCTGATTGATTTTTAAATGCGTTTTTGGG  
 AGAACTTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTATAATTACATCTG  
 TGATTTCTGAACATAATGGTGCTAATTCAGAGAAATGGAAAGTGAAAGTGAGATTCTCTGTTGTCTCGGCATTCC  
 AACTTTTTCTCTTTGTTTTTGTCCAGTGTTCATTTGAATATGTCTGTTCTATAAAATAAATTTTTTAAGAATAA

09978299 "101501

## FIGURE 155

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329

><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLLALAALLAFVLSLQFFHLIPVSTPKNGMSSKSRKRIMPDPVTEPPVTDVY  
EALLYCNIPPSVAERSMEGHAPHHFKLVSVHVFIRHGDYPLYVIPKTKRPEIDCTLVANRKP  
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK  
KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP  
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSM LCHFCHNVSFPC  
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQ TIGRMQRATEGRKEELF  
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSHSVRILYNGVDVTFHTSF  
CQDHHKRSPKPMCPLNLVRFVKRDMFVALGGSGTNYYDACHREGF

**Signal sequence:**

amino acids 1-18

09078299-101501  
TOSTOT" 65284660



# FIGURE 156

AAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCCATCCCCTTTTGAAGAACAGTACTGTGGA  
GCTATTTAAGAGATAAAAAACGAAATATCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC  
GCCGCTGTTTACCAATCGGGGAGAGAAAAAGCGGAGATCCTGCTCGCCTTGCACGCGCCTGAAGCACAAGCAGAT  
AGCTAGGAATGAACCATCCCTGGGAGTATGTGGAAACAACGGAGGAGCTCTGACTTCCCAACTGTCCCATTCTAT  
GGGCGAAGGAACTGCTCCTGACTTCAGTGGTTAAGGGCAGAATTGAAAATAATTCTGGAGGAAGATAAGAATGAT  
TCCTGCGCGACTGCACCGGACTACAAAGGGCTTGTCTGCTGGGAATCCTCCTGGGGACTCTGTGGGAGACCGG  
ATGCACCCAGATACGCTATTCACTTCCGGAAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGGACCT  
GGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCCAGAGGTAGGACGCAGCTTTTCGCCCT  
GAATCCGCGCAGCGGCAGCTTGGTCACGGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTG  
TCAATTAAATCTAGACATTCTGATGGAGGATAAAGTGAAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTAA  
CGACAATGCGCCTTACTTTCTGTGAAAGTGAATTAGAAAATAAAAATTAGTGAAAATGCAGCCACTGAGATGCGGTT  
CCCTCTACCCACGCTTGGGATCCGGATATCGGGAAGAACTCTCTGCAGAGCTACGAGCTCAGCCCGAACACTCA  
CTTCTCCCTCATCGTGCAAAATGGAGCCGACGGTAGTAAGTACCCGAATTGGTGCTGAAACGCGCCCTGGACCG  
CGAAGAAAAGGCTGCTCACCACTGGTCTTACGGCTCCGACGGGGGCGACCCGGTGCGCACAGGCACCGCGCG  
CATCCGCGTGATGGTTCTGGATGCGAACGACAACGCACACGCGTTTGCTCAGCCCGAGTACCGCGCGAGCGTTCC  
GGAGAATCTGGCCTTGGGCACGCAGCTGCTTGTAGTCAACGCTACCGACCCCTGACGAAGGAGTCAATGCGGAAGT  
GAGGTATTCTTCCGGTATGTGGACGACAAGGCGGCCCAAGTTTTCAAAGTATGTAATTAGGGGACAATATC  
AACATAGGGGAGTTGGACCACGAGGAGTCAAGATTCTACAGATGGAAGTGCAAGCAATGGATAATGCAGGATA  
TTCTGCGCGAGCCAAAGTCTGATCACTGTTCTGGACGTGAACGACAATGCCCGAGAAGTGGTCCCTCACCTCT  
CGCCAGCTCGGTTCCCGAAAACTCTCCAGAGGGACATTAATTGCCCTTTTAAATGTAAATGACCAAGATTCTGA  
GGAAAACGGACAGGTGATCTGTTTCATCCAAGGAAATCTGCCCTTTAAATTAGAAAAATCTTACGGAAATTACTA  
TAGTTTAGTCACAGACATAGTCTTGGATAGGGAACAGGTTCTAGCTACAACATCACAGTGACCGCCACTGACCG  
GGGAACCCCGCCCTATCCACGGAACTCATATCTCGCTGAACGTGGCAGACACCAACGACAACCCGCGCGTCTT  
CCCTCAGGCCCTCTATTCCGCTTATATCCAGAGAAATCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCCCA  
CGACCCCGACTGTGAAGAGAACGCCAGATCACTTATCCCTGGCTGAGAACACCATCCAAGGGGCAAGCCTATC  
GTCCTACGTGTCCATCAACTCCGACACTGGGGTACTGTATGCGCTGAGCTCCTTCGACTACGAGCAGTTCCGAGA  
CTTGCAAGTGAAAGTGATGGCGCGGGACAACGGGCACCCGCCCTCAGCAGCAACGTGTGTTGAGCCTGTTTCGT  
GCTGGACCAGAACGACAATGCGCCCCGAGATCCTGTACCCCGCCCTCCCCACGGACGGTTCCACTGGCGTGGAGCT  
GGCTCCCCGCTCCGCGAGAGCCCGGTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCCGGCCAGAACGC  
CTGGCTGTCTACCGTCTGTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAGGTGCG  
CACGGCGCGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCCTCGTAGTGGCCGTCCAGGACCACGGCCAGCC  
CCCTCTCTCCGCCACTGTACGCTCACCGTGGCCGTGGCCGACAGCATCCCCAAGTCTGGCGGACCTCGGCAG  
CCTCGAGTCTCCAGCTAACTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCCGCGGTCTCCTG  
CGTCTTCTTGGCCTTCGTCATCTTGTCTGCTGGCGCTCAGGCTGCGGCGCTGGCACAAGTCACGCCTGCTGCAGGC  
TTCAGGAGGCGGCTTGACAGGAGCGCCGGCGTGCACCTTGTGGGCGTGACGGGGTGACGGCTTTCCTGCAGAC  
CTATTCCACGAGGTTTCCCTCACCACGGACTCGCGGAAGAGTCACTGATCTTCCCCCAGCCCAACTATGCAGA  
CATGCTCGTCAGCCAGGAGAGCTTTGAAAAAAGCGAGCCCTTTTGTGTGAGGTGATTGGGTATTTTCTAAAGA  
CAGTCATGGGTAAATTGAGGTGAGTTTATATCAAATCTTCTTTCTTTTTTTTTTAATTGCTCTGTCTCCCAAGC  
TGGAGTGCAGCGTACGATCATAGCTCACTGCGGCCTCAAACCTCTAGGCTCAAGCAATTATCCCACCTTTGCCT  
CCGGTGTAAACAGGACTACAGGTGCAAGCCACCTACTGTCTGCCTATCTATCTATCTATCTATCTATCTATCTAT  
CTATCTATCTATCTATCTATCTATCTTCTTGTACAGACGGGAGTCTCACGCCTGTAATCCAGTACTTTGGGAGGC  
CGAGGCGGGTGGATCACCTGAGGTTGGGAGTTTGGAGCCAGCTGACCAACATGGAGAAACCCGCTCTATACTAA  
AAAAATACAAAATTAGCCGGGCGTGGTGGTGCATGTCTGTAATCCAGCTACTTGGGAGGCTGAGTCAGGAGAAT  
TGCTTTAACTTGGGAGGTGGAGGTTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCCTGGGCAACAAGAGTG  
AAACTCTATCTCA

0978299 101504

## **FIGURE 157**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVPEELEKGSRVGDISRDLGLEPRELAER  
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVR  
DINDNAPYFRESELEIKISENAATEMRFPPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA  
DGSKYPELVVKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFAPQPEYR  
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSPRYVDDKAAQVFKLDCNSGTISTIGELDHE  
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLNVN  
DQDSEENGQVICFIQGNLPFKLEKSYGNYYSLVTDIVLDREQVPSYNITVTATDRGTPPLST  
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVSLVSVTAHDPDCEENAQITYSLAENTI  
QGASLSSYVSINSDTGVLIALSSFDYEQFRDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDN  
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVAVDRDSGQNAWLSYRLLKASEPGLFSVG  
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTTLTVAVADSIPOVLADLGSLESPA  
NSETSDLTLYLVVAVAAVSCVFLAFVILLALLRLRRWHKSRLQLASGGGLTGAPASHFVGVD  
GVQAFLLQTYSHVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLSGDSVFSKDSHGL  
IEVSLYQIFFLFFNCVSQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDYZCKPPTVCLS  
IYLSIYLSIYLSIYLLLSCTDGS�TPVIPVLWEAEAGGSPEVGSLRPA

### **Signal sequence:**

amino acids 1-30

### **Transmembrane domains:**

amino acids 693-711, 809-823, 869-888

09978299 "101501

## FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG  
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA  
TCAGTAGGTGACCCCGCCCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCCGACCTCGT  
GCGGCCAAGACGTGGATGTTCTTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC  
ACAGGAGGACAAGGTGCTGGGGGGTTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG  
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAAGTGGCAACTGGGTCTT  
ACAGCTGCCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA  
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTTCAGTCCATCCCACACCCCTGCTACAACA  
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC  
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG  
CACCGTCTCAGGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTTCCTGACACTCTCAACT  
GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA  
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG  
CCCCCTGGTGTGTGATGGTGCCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA  
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC  
ATAGGCAGCAAGGGCTGGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACCTCT  
CTGGTTC

09978299.101504

## **FIGURE 159**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL  
VGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIPHPCYNSSDVEDHNHDLMLL  
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCED  
AYPGQITDGMVCAGSSKGADTCQGDGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRY  
LDWIKKIIGSKG

### **Important Features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 51-71

#### **N-glycosylation site.**

amino acids 110-113

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 69-74 and 207-217

#### **Tyrosine kinase phosphorylation site.**

amino acids 182-188

#### **Kringle domain proteins motif**

amino acids 205-217

09978299.101501  
TDSFOT" 6628/660

## FIGURE 160

GGCGCCGGTGACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCCGC  
CGCGCCGCCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGCCCCGCGCCCCG  
GCCCCGCGCCAGGTGAGCGCTCCGCCCGCCGCGAGGCCCGCCCCGGCCCCCGCCCCGCCCCG  
CCCCGGCCGGCGGGGGAACCGGGCGGATTCTCGCGCGTCAAACACCTGATCCCATAAAAC  
ATTTCATCCTCCCGGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCCGCCGCGCCCTCG  
CCCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCCAGCCAGAGCCGGGCGGAGC  
GGAGCGCGCCGAGCCTCGTCCCGCGGCCGGGCGGGGCCGGGCGGTAGCGGCGGCGCCTGGA  
TGCGGACCCGGCCGCGGGGAGACGGGCGCCCCGCCCGAAACGACTTTCAGTCCCCGACGCGC  
CCCGCCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG  
CTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCCAGGTGCCTGCGTATGCTACAATGA  
GCCCAAGGTGACGACAAGCTGCCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTG  
CTGCCAGCCAGCGCATCTTCTGACGGAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC  
CGTGCTGCCGCAACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGC  
GGCTGCCTTCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC  
GGTCTGTGGACCCTGCCACATTCCACGGCCTGGGCCGCCTACACACGCTGCACCTGGACCGC  
TGCGGCCTGCAGGAGCTGGGCCCGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTA  
CCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCA  
CACACCTCTTCTGACGGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTG  
CACAGCCTCGACCGTCTCCTACTGCACCAGAACCGCGTGGGCCATGTGCACCCGCATGCCTT  
CCGTGACCTTGGCCGCCTCATGACACTCTATCTGTTGCCAACAATCTATCAGCGCTGCCCA  
CTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG  
TGTGACTGCCGGGCACGCCCCACTCTGGGCCTGGCTGCAGAAGTTCCGCGGCTCCTCCTCCGA  
GGTGCCCTGCAGCCTCCCGCAACGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATG  
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCCTCTGGACCCGCGAGGGCCACC  
GATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGT  
ACTGGAGCCTGGAAGACCAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTG  
ACAGCCCGCCGGGCAACGGCTCTGGCCACGGCACATCAATGACTCACCTTTGGGACTCTG  
CCTGGCTCTGCTGAGCCCCCGCTCACTGCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTT  
CCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCGCACCCGCAGCCACT  
GCCGTCTGGGCCAGGCAGGCAGCGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCC  
CTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGGCCTGGCGCTGGTGCTGTGGACAGTGCT  
TGGGCCCTGCTGAACCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATAC  
GGGGTCTCTCTCCACGCGCCCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAG  
GTCCTCCCTGATGGACGCCTGCCGCCCGCCACCCCCATCTCCACCCCATCATGTTTACAGGG  
TTCGGCGGCAGCGTTTGTTCAGAACGCCGCCTCCACCCAGATCGCGGTATATAGAGATAT  
GCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAA  
AAAA

09973299 101501

## FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184

><subunit 1 of 1, 473 aa, 1 stop

><MW: 50708, pI: 9.28, NX(S/T): 6

MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI  
FLHG NRISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDP  
TFHGLGRLHTLHLDRCLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH  
GNRISSVPERAFRGLHSLDRLLLHQNRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAP  
LRALQYLRRLNDNPWVCDRCARPLWAWLQKFRGSSSEVPCLPQRLAGRDLKRLAANDLQGCA  
VATGPYHPIWTGRATDEEPLGLPKCCQPDAAADKASVLEPGRPASAGNALKGRVPPGDSPPGN  
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA  
GSGGGGTGDSESGALPSLTCSLTPLGLALVLWTVLGPC

**Important features:**

**Signal peptide:**

amino acids 1-26

**Leucine zipper pattern.**

amino acids 135-156

**Glycosaminoglycan attachment site.**

amino acids 436-439

**N-glycosylation site.**

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

**VWFC domain**

amino acids 411-425

09978299.101501  
TOSTOT" 55282660

# FIGURE 162

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCCTCTGGAGAGGACTAC  
TCACTGGCATATTTCTGAGGTATCTGTAGAATAACACAGCCTCAGATACTGGGGACTTTAC  
AGTCCACAGAACCGTCCTCCCAGGAAGCTGAATCCAGCAAGAACAATGGAGGGCCAGCGGGA  
AGCTCATTTGCAGACAAAGGCAAGTCCTTTTTTCTCTTTTGGGCTTATCTCTGGCG  
GGCGCGGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAAACTGAGGGCAGCTCCTTTGTAC  
CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGGTTAGGGTTG  
TTTCCAGAGGGAAACAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTTGTTGCTAAAT  
GAGAAATTGGACCGTGAGGATCTGTGCGGTACACAGAGCCCTGTGTGCTACGTTTCCAAGT  
GTTGCTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC  
ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCCTCCTGGG  
ACTACGTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA  
TATAATCAGCCCCAACTCCTATTTTCGGGTCTCACC CGCAAACGCAGTGATGGCAGGAAAT  
ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA  
CTCACAGCACTGGATGGTGGCTCTCCGCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT  
CCTGGATGTCAACGATAATGCCCTGAATTTGAGCAGCCTTTCTATAGAGTGACAGATCTCTG  
AGGACAGTCCGGTAGGCTTCTGGTGTGAAGGTCTCTGCCACGGATGTAGACACAGGAGTC  
AACGGAGAGATTTCTATTCACTTTTCCAAGCTTCAGAAGAGATTGGCAAACCTTTAAGAT  
CAATCCCTTGACAGGAGAAATTGAACTAAAAAAACAACCTCGATTTCGAAAACTTCAGTCCT  
ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGGAAAATGCACCGTTCTGATT  
CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTACAGCCCAAT  
ACCTGAGAACGCGCCTGAAACTGTGGTTGCACTTTTCAAGTGTTCAGATCTTGATTACAGGAG  
AAAATGGGAAAATTAGTTGCTCCATTGAGGAGGATCTACCCTTCTCCTGAAATCCGCGGAA  
AACTTTTACACCCTACTAACGAGAGACCACTAGACAGAGAAAGCAGAGCGGAATACAACAT  
CACTATCATGTCACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC  
TGATCGCCGATGTCAATGACAACGCTCCCGCTTACCCAAACCTCCTACACCTGTTCTGTC  
CGCGAGAACAACAGCCCCGCCCTGCACATCCGCGAGCTCAGCGCTACAGACAGAGACTCAGG  
CACCAACGCCCAGGTCACTACTCGCTGCTGCCGCCAGGACCCGCACCTGCCCTCACAT  
CCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTCCGCCCTCAGGTCTCTGGACTACGAG  
GCCCTGCAGGGGTTCCAGTTCGCGCTGGGCGCTTCAGACCACGGCTCCCCGGCGCTGAGCAG  
CGAGGCGCTGGTGCGCGTGGTGGTGTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACC  
CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCGGAGCCGGGCTAC  
CTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTCTGTACCA  
GCTGCTCAAGGCCACGGAGCTCGGTCTGTTCCGGCGTGTGGGCGCACAAATGGCGAGGTGCGCA  
CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGTGGTCAAGGAC  
AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCCTGGTGGACGGCTTCTC  
CCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCGACCCAGGCCAGGCCGACTTGCTCACCG  
TCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTTTTCGGTGTCTCTGTTT  
GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCCCTCGGTGGGTGCTGCTTGGTGCCGA  
GGGCCCCCTTCCAGGGCATCTTGTGGACATGAGCGGCACCAGGACCCTATCCAGAGCTACC  
AGTATGAGGTGTGTCTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTTCCTGAAGCCGATT  
ATCCCAACTTCCCTCCCCAGTGCCCTGGGAAAGAAATACAAGGAAATTCTACCTTCCCCAA  
TAACTTTGGGTTCAATATTCAGTGAACCATAGTTGACTTTTACATTCCATAGGTATTTTATTT  
TGTGGCATTTCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGTAATATTGTACGGAT  
TTACTCTTGATTTTTCTCATGTTCTTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT  
CCTGGTCTT

097829-101501

## **FIGURE 163**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314

<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKLICRQRQVLFSLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR  
RGVRVVSARGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRQVLLSPFEFFQAEQV  
IDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR  
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY  
RVQISEDSPVGFLVVKVSATDVDGTGVNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF  
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPENAPETVVALFSVS  
DLDSGENGKISCISIQEDLPFLKSAENFYTLTTERPLDRESRAEYNITITVTDLGTPMLITQ  
LNMTVLIADVNDNAPAFQTSTYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLPPQDP  
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVVLDANDNS  
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELGFLGVWAH  
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAA  
ADLLTVYLVVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMSGTRT  
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFPPQCPGKEIQGNSTFPNNFGFNIQ

### **Important features:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 685-712

#### **Cadherins extracellular repeated domain signature.**

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 285-292

#### **N-glycosylation site.**

amino acids 418-421, 436-439, 567-570 and 786-789

09978299.101501



## FIGURE 164

ACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCGCGTAGCCGTGC  
GCCGATTGCCTCTCGGCCTGGGCAATGGTCCCGGCTGCCGGTCGACGACCGCCCCGCGTCAT  
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTG  
AGGTTGCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCCCTCTCCAGGTG  
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC  
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG  
TGATTCCTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT  
GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG  
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG  
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG  
GAGAGAAACATTACAGGATTAGAAAAATTTCACTCTGAAAATTTTAAATATGTCACAGGACCT  
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGT  
GCCGCTTTTCTGCCAGTTTGGCCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT  
CACTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC  
TGTTCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATAACAGATC  
GAACACTGGAAACACTGAAAATCTTCATTTTAAATCAGACAGGTATAGAAGCCAAGAAGAAT  
GTGGTGGTAACTCAAGCCGACCAAATAGGCCCTCTTCCCAGCACTTTGATAAAAAGTGTGGA  
CTGGTTGCTTGATTTTCCCTTATTCTTTTTTAATTAGTTTTATTATGTATGCTACCATTCGAA  
CTGAGAGTATTCGGTGGCTAATTCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT  
GAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA  
CATTTTCTCCAGTGACGTGTTGACTTGAACTTCAGGCAGATTAAAAGAATCATTTGTTGAA  
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC  
AAAAATATTCAATAG

09978299-101504

## **FIGURE 165**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333

><subunit 1 of 1, 360 aa, 1 stop

><MW: 39885, pI: 4.79, NX(S/T): 7

MVPAAGRRPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE  
ELLHDPMGQDRAAEEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTCTGAGGAEDSRC  
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE  
NFTLKIILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS  
QHSSLSTRFGTVAVPNILLFQGAKPMARFNHTDRTLETCLKIFIFNQTGIEAKKNVVVTQADQ  
IGPLPSTLIKSVDWLLVFSLFFLISFIMYATIRTESIRWLIPGQEQEHVE

### **Important features:**

#### **Signal peptide:**

amino acids 1-25

#### **Transmembrane domain:**

amino acids 321-340

#### **Homologous region to dilsufide isomerase**

amino acids 212-302

#### **N-glycosylation site.**

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281  
and 293-296

#### **Thioredoxin domain**

amino acids 211-227

00978293.101501  
105101"55287550

## FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCACGATGCTGCAGGGCCCTGGCT  
CGCTGCTGCTGCTCTTCCTCGCCTCGCACTGCTGCCTGGGCTCGGCGCGGGGCTCTTCCTC  
TTTGGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA  
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCAACCTGCTGGGCCACGAGACCA  
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTTCATGAAGCAGTGCCACCCG  
GACACCAAGAAGTTCTGTGCTCGCTCTTCGCCCCCGTCTGCCTCGATGACCTAGACGAGAC  
CATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGTTCATGTCCG  
CCTTCGGCTTCCCCTGGCCCGACATGCTTGAGTGCGACCGTTTCCCCCAGGACAACGACCTT  
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG  
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG  
ATTTTGCCTGAAAATAAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAATCATC  
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA  
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAGTGCACCTGTGAGGAGATGAACGACATCAACG  
CGCCCTATCTGGTTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG  
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTTA  
GTCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTTCTGCTCC  
GGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT  
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTCTGAGTTATAAGGCCACAGGAGTG  
GATAGCTGTTTTACCTAAAGGAAAAGCCCACCCGAATCTTGTAGAAATATTCAAACCTAATA  
AAATCATGAATATTTTAA

09978299 " 101501

## FIGURE 167

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920

><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

MLQGPGSLLLLFLASHCCLGSAAGLFLFGQPDFSYKRSNCKPIPVNLQLCHGIEYQNMRLPN  
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDLDETIQPCHSVCVQVKDR  
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM  
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGVSEKDLKKSVLWLKDSLQCTCE  
EMNDINAPYLVMGQKQGGELVITSVKRWQKGQREFKRISRSIRKLQC

**Important features:**

**Signal peptide:**

amino acids 1-20

**Cysteine rich domain, homologous to frizzled N terminus**

amino acids 6-153

09978299 101501

## FIGURE 168

GTGGAGGCCCGCCGACGATGGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG  
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTGCTCGCGATC  
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT  
TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG  
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTCGGGCTCCGTGCGGCG  
ACCATCCTGGGTGCGTGGCTGAACTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT  
TGTTGGGACCCAAAACCCATTTGCCTTCCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC  
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTTGGTTCCCAGAGCACCAGCGA  
GCCACGGCCAACATGCTCGCCACCATGTGCAACCCTCTGGGCGTCCTTGTGGCCAATGTGCT  
GTCCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATACCATCC  
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACCCTG  
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCCTGGATGGGCTCAAGCTGCAGCT  
CATGTGGAACAAGGCCTATGTCATCCTGGCTGTGTGCTTGGGGGGAATGATCGGGATCTCTG  
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC  
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCCCTA  
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG  
CCTGCGTGCCCTTTGCCCTGGTGTCCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC  
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTCTGA  
GTGTTCTTCCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG  
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCTTG  
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG  
CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC  
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG  
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCCTGGGGCCCAGCACGGCGACTCCGGA  
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGGAGCCCCACCCAGCCT  
GCCACCGAGCGACTCCCCGTGCGCAAGGCCCAGCAGCCACCGACGCGCCCTCCCGCCCCGGC  
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT  
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTTAGTCCAGGTTGCCCCGCCACATCGA  
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT  
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

## **FIGURE 169**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988

><subunit 1 of 1, 560 aa, 1 stop

><MW: 58427, pI: 6.86, NX(S/T): 2

MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV  
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN  
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQ RATANMLATMSNPLGVLVANVLS PVLV  
KKGEDIPLMLGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA  
YVILAVCLGGMIGISASFSALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK  
HFTEATKIGLCFLSLACVPFALVSQ LQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV  
GEGAATGMIFVLGQAE GILIMLMTALT VRRSEPSLSTCQQGEDPLDWTVSLLL MAGLCTFF  
SCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG  
ASLEDPRGPGSPHPACHRATPRAQGPAA TDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

### **Important features:**

#### **Signal peptide:**

amino acids 1-44

#### **Transmembrane domains:**

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,  
280-300, 318-337, 341-357, 375-387, 420-441

#### **N-glycosylation site.**

amino acids 40-43 and 43-46

#### **Glycosaminoglycan attachment site.**

amino acids 468-471

09978299.10501  
"66282660"

# FIGURE 170

GTCCACATCTGCTCAACTGGGTGAGTCCCTCTTAGACCAGCTCTTGTCATCATTTGCTGAAGTGGACCAAC  
TAGTTCCCCAGTAGGGGGTCTCCCTGGCAATTCTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA  
TGGCCTTGCTTGGGGTCTGCTTGTTCATAATCATCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGG  
AAGGAGCACGGGGCTGATCAAGCCATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAACTCTAGTGGTT  
TCTGAATCTAGCCCACTTGGCGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG  
CTACTTATTTCTTTTAGGGGATTGTGAGGAGGTGACCACTCTCACGGTGAATACCAAGTGTGAGAGGAAGTGCC  
ATCTGGTACAGTGATCGGGAAGCTGTCCCAGGAACCTGGGCCGGGAGGAGAGGCGGAGGCAAGCTGGGGCCGCTT  
CCAGGTGTTGACGCTGCCTCAGGCGCTCCCCATTGAGGTGACTCTGAGGAAGGCTTGCTCAGCACAGGCAGGCG  
GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGATCCCTGCCTGGTTTCTTTGATGTGCTTGCCACAGGGGATT  
GGCTCTGATCCATGTGGAGATCCAAGTGTGACATCAATGACCACCAGCCACGGTTTCCCAAAGGCGAGCAGGA  
GCTGGAAATCTCTGAGAGCGCCTCTCTGCGAACCCTGGATCCCCCTGGACAGAGCTCTTGACCCAGACACAGGCC  
TAACACCCTGCACACCTACACTCTGTCTCCAGTGGACACTTTGCCTTGGATGTGATTGTGGGCCCTGATGAGAC  
CAAACATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAATCCATTCAATTTTTGATCTGGTGTAACTGC  
CTATGACAATGGGAACCCCCCAAGTCAAGTACCAGCTTGGTCAAGGTCAACGTCTTGGACTCCAATGACAAATAG  
CCCTGCGTTTGTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAACT  
GACCGCCACAGACCCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCTCAGTAAGCACATGCCTCCAGAGGT  
GCTGGACACCTTCACTATTGATGCCAAGACAGGCAGGTCACTTCTGCTCGACCTCTAGACTATGAAAAGAACCC  
TGCTTACGAGGTGGATGTTGAGCAAGGACCTGGGTCCCAATCCTATCCAGCCCATGCAAGTTCTCATCAA  
GGTTCTGGATGTCAATGACAACATCCCAAGCATCCACGTGACATGGGCCCTCCAGCCATCACTGGTGTCAAGAGC  
TCTTCCCAAGGACAGTTTTATTGCTCTTGTGATGGCAGATGACTTGGATTGAGGACACAATGGTTTGGTCCACTG  
CTGGCTGAGCCAAGAGCTGGGCCACTTCAAGGTGAAAAGAACTAATGGCAACACATACATGTTGCTAACCAATGC  
CACTGAGACAGAGAGCAGTGGGCCAAATATACCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC  
AGCCAAGAAACAGCTCAGCATTGATGACATCAACGACAATGCACCTGTGTTTGAAGAAAGCAGGTATGA  
AGTCTCCAGCGGGGAAAACAACCTTACCTCTCTTCACTTACCATCAAGGCTCATGATGCAGACTTGGGCAT  
TAATGAAAAGTCTCATACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTAGCTATTGACTCCAACACAGGAGA  
GGTCACTGCTCAGAGGTCACTGAACATGAAGAGATGGCCGGCTTTGAGTTCCAGGTGATCGCAGAGGACAGCGG  
GCAACCCATGCTTGCATCCAGTGTCTCTGTGTGGGTGAGCCTCTTGGATGCCAATGATAATGCCCCAGAGGTGGT  
CCAGCCTGTGCTCAGCGATGGAAGGCCAGCCTCTCCGTGCTTGTGAATGCCCTCCACAGGCCACCTGCTGGTGGC  
CATCGAGACTCCCAATGGCTTGGGCCAGCGGGCACTGACACACCTCCACTGGCCACTCACAGCTCCCGGCCATT  
CCTTTTGACAACCATTGTGGCAAGAGATGCAGACTCGGGGGCAATGGAGAGCCCTTACAGCATCCGCAATGG  
AAATGAAGCCCACCTCTTCACTCTCAACCTCATACGGGGCAGCTGTTGCTCAATGTACCAATGCCAGCAGCCT  
CATTGGGAGTGAGTGGGAGCTGGAGATAGTAGAGGACCAGGGAAGCCCCCTTACAGACCCGAGCCCTGTT  
GAGGGTCATGTTTGTCAACAGTGTGGACCCTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTGAT  
GCTGACGGTGATCTGCCTGGCTGTACTGTTGGGCATCTTGGGTTGATCCTGGCTTTGTTTATGTCCATCTGCCG  
GACAGAAAAGAAGGACAAACAGGGCTACAACCTGTGAGGAGCCAGTCCACCTACCGCCAGCAGCCCAAGAGGCC  
CCAGAAACACATTGAGAAGGCAGACATCCACCTCGTGCTGTGCTCAGGGGTGAGGAGGCTTGTGAAGT  
CGGGCAGTCCACAAAGATGTGGACAAGGAGGCGATGATGGAAGCAGGCTGGGACCCCTGCTGAGGCCCCCTT  
CCACCTACCCCGACCTGTACAGGACGCTGCGTAATCAAGGCAACAGGAGACCCGGCGGAGAGCCGAGAGGT  
GCTGCAAGACACGGTCAACCTCTTTCAACCATCCAGGCGAGGGAATGCCCTCCCGGGAGAACCTGAACCTTCC  
CGAGCCCCAGCCTGCCACAGGCCAGCCAGTTCCAGGCCTCTGAAGGTTGAGGAGCCCCACAGGGAGGCTGGC  
TGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCACAGCCTCTCTGCAACCTGAGACGGCAGCGACATCT  
CAATGGCAAAGTGTCCCCTGAGAAAGAATCAGGGCCCCGTGAGATCCTGCGGAGCCTGGTCCGGCTGTCTGTGGC  
TGCCTTCCCGAGCGGAACCCCGTGGAGGAGCTCACTGTGGATTCTCTCTGTTTACAGCAATCTCCAGCTGCT  
GTCCTTGTGCTGATCAGGGCCAATTCCAGCCCAAACCAAACACCGAGGAAATAAGTACTTGGCCAAGCCAGGAGG  
CAGCAGGAGTGCAATCCAGACACAGATGGCCCAAGTGCAAGGGCTGGAGGCCAGACAGACCCAGAACAGGAGGA  
AGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGAAGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCC  
CAGCACAGGTCTGGCCCTGGACCGGCTGAGCGCCCCCTGACCCGGCTGGATGGCGAGACTCTCTTTGCCCTCAC  
CACCAACTACCGTGACAATGTGATCTCCCCGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGTTCCG  
CAAGGCAGAGGCACAGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTCTCGGAGATGAGCTCACT  
GCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCTGAGGAGCCGCTCCGAGGCGCTGCGGCGGCTCTCGGT  
CTGCGGGAGGACCTCAGTTTAGACTTGGCCACCAAGTGCAGCCTCAGGCATGAAAGTGCAAGGGACCCAGGTGG  
AAAGACGGGGACTGAGGGCAAGAGCAGAGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC  
CTGGATCCAAGAACCAGGGGCTGAGGATCTGTGGACAAGAGCTGGTTTCTAAAATCTTGTAACTCACTAGCTAG  
CGGCGGCTTGAAGCTTTAGGGTGACTGATGTACCCCAACAGAGGAGGCAAGAGCCCCAGGACTAACAGCTGAC  
TGACCAAAGCAGCCCCCTTGTAAAGCAGCTCTGAGTCTTTTGGAGGACAGGGACGGTTTGTGGCTGAGATAAGTGT  
TCCTGGCAAAACATATGTGGAGCACAAAGGTGAGTCCCTTGGCAGAACAGATGCCACGGAGTATCACAGGCAGG  
AAAGGGTGGCCTTCTTGGGTAGCAGGAGTCAAGGGGTGTACCTGGGGGTGCCAGGAATGCTCTCTGACCTAT  
CAATAAGGAAAAGCAGTAAAAAAAAAAAAAAAAAAAAA

0997899 101501

## FIGURE 171

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331

<subunit 1 of 1, 1184 aa, 1 stop

<MW: 129022, pI: 5.20, NX(S/T): 5

MMQLLQLLLGLLGGPYLFLGDCQEVTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA  
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFDVLATGDLALIHVEIQ  
VLDINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNLTHTYTLSPSEHFALDVIV  
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSNDNSPAFAESS  
LALEIQEDAAPGTLLIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPL  
DYEKNPAYEVDVQARDLGPNIPIAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSF  
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLAQQD  
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHDADLGINGKVS  
YRIQDSPVAHLVAIDSNTGEVTAQRSLNYEEMAGFEFQVIAEDSGQPMCLASSVSVVWSLLDA  
NDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPPLATHSSRPFLTTT  
IVARDADSGANGEPLYSIIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIIVVEDQGS  
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK  
KDNRAYNCREAESTYRQQPKRPQKHQKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEA  
GWDPCQLQAPFHLTPTLYRTLNRQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENLNLPPEP  
QPATGQPRSRPLKVAGSPTGRLAGDQGSSEAPQRPASSATLRRQRHLNGKVSPEKESGPRQ  
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKEGGS  
RSAIPD TDGPSARAGGQTDPEQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPD  
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL  
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSDLATSAAAGMKVQGDPPGKTGTGEGKSRGSS  
SSSRCL

### **Important features:**

#### **Signal peptide:**

amino acids 1-13

#### **Transmembrane domain:**

amino acids 719-739

#### **N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

#### **Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

097829.101501



# FIGURE 172

CGGACGCGTGCGGCGGACGCGTGCGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGG  
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG  
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT  
CCCAGATACTATTTTTTGGATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT  
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCAATTTCTTGACCAT  
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT  
GGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTTTACATTGGC  
TATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTTCTGTCTCTT  
ATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCCCATTTCTCAGCCCAA  
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTGGTGTGATTGGAGTGACTCTC  
ATGGCTCTTCTTTCTGGATTTGGTGTGTCAACTGCCCATACACTTACATGTCTTACTTCCT  
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA  
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA  
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGG  
AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC  
TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC  
AAGGGGAAATATTTTAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAATTTT  
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCAAGAGGGCA  
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATT  
TCCTTCATTCTTGTTGGAATAATCATCGTCCATCCATCAGAGGATTGCTGATCACTCTTAC  
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCCTGCTATTAGCAC  
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA  
TACCGCACCATAATCACTGAAGTCCTTGAGAACTGCAGTTCAACTTCTATACCGTTGGTT  
TGATGTGATCTTCCTGGTCAGCGCTCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAAC  
AGGCACCAGAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGT  
GGTTTCAAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAAC  
AAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGCATACTCCTTCCCCGTCAGGTGATA  
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA  
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAACTAA  
AGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT  
AGGATTTCCGTTTTTAAGGTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT  
AAAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCG  
ACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

09978299.101501

## **FIGURE 173**

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFASFCTMFELIIFEI  
LGVLNSSSRYPFHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFF  
WKLGDPPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI  
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ  
QEVDAL EELS RQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF  
DRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAIS  
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQNFYHRWFDVIFLVSA  
LSSILFLYLAHKQAPEKQMAP

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

#### **N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

#### **Eukaryotic cobalamin-binding proteins**

amino acids 151-160

0978259 101501  
TOSTOT 55284660

## FIGURE 174

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA  
TCATGATTACCTCCCNGANACTATTTTTTTGGATTGTTGGGTGGCTTTTCTTCNGCGCCAATGTT  
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT  
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT  
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT  
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAACAACGACTGCTTTTTT  
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

FOUO 101501 66282660

## FIGURE 175

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC  
TTTNTTGAATTCCGGGTTNNGNATACCTTCCCAGAAAATATTTTTTGGATTTGGGGTAGNTT  
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT  
NTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG  
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC  
CTGGTTTTCATGGTGCCTTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA  
TAAACAACGACTGCTTTTTTCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTTGAAAN  
TAGGAGATCCCTTCCCATTCCTC

09078299 101501  
FOUO 1628/660



## **FIGURE 177**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL  
QPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWL  
GVSVRSQGPQGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDDGGGEWKFC  
RPGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGRTARVELCAQGSADLAHLDDGPYEA  
GGEKEQDPRLLIPVPANSYFGFSIDSGKGLVRAEELSFVAGAPRANHKGAVVILRKDSASRLV  
PEVMLSGERLTSGFGYSLAVADLNSDGWPDLLVIGAPYFFERQEELGGAVVYVLNQGQHWAGI  
SPLRLCGSPDSMFGISLAVLGDNLNQGDFPDIAVGAPFDGDGKVFIYHGSSLGVVAKPSQVLE  
GEAVGIKSFYSLSGSLDMDGNQYPDLLVGLADTAVLFRARPILHVSHEVSIAPRSIDLEQ  
PNCAGHSVCVDLRVCFYSYIAVPSSYSPTVALDYVLDADTDRLRGQVPRVTFLSRNLEPK  
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSTSLQTPRLRRQAPGQGLPPVAP  
ILNAHQSTQRAEIHFLKQCGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA  
LSGQPVIGLELMVTNLPSPDPAQPQADGDDAHEAQLLVMLPDSLHYSVGRALDPAEKPLCLSN  
ENASHVECELGNPMKRGAQVTFYLILSTSGISIIETTELEVELLLATISEQELHPVSARARVF  
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKEYEVTVSNQGQSLRTLGS AFLNIM  
WPHEIANGKWL LYPMQVELEGGQGPQKGLCSRPNIHLHDVDSRDRRRRELEPPEQQEPGE  
RQEPSMSWWPVSSAEKKKNITLDCARGTANCVVFSCLYSFDRAAVLHVWGRLWNSTFLEEY  
SAVKSLEIVVRANITVKSSIKNLMLRDASTVIVMVYLDPMVVAEGVPWWVILLAVLAGLL  
VLALLVLLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGTILRNNWGSPREGP  
DAHPIAADGHPGLGPDGHPGPGTA

### **Important features:**

#### **Signal peptide:**

amino acids 1-33

#### **Transmembrane domain:**

amino acids 1040-1062

#### **N-glycosylation sites.**

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

#### **Integrins alpha chain proteins.**

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-  
407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408  
and 1031-1047

0976299-101501  
TOSTOT" 55232550

## FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCAGA  
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT  
CACAAACAAGATGCTCAAGGTGTCAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTGCACTCA  
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGCGGTCCGACGGCGGTAATTTTC  
TGGATGATAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC  
AAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACCTGGAGTCCAGGAAAACCCTTCGA  
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT  
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG  
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG  
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTTCAGATGGTCATACCTACTCTTTTCAGTGCA  
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC  
CCATGTCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT  
GGAGTTCAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAA  
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTCGATACCAGCATC  
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAACAGACTTGATACAAACTATGACCT  
GCTATTGGACCAGTCAGAGCTCAGAAGCATTACCTTGATAAGAATGAACAGTGTACCAAGG  
CATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC  
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA  
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC  
CAACACAATGTCATGGCAGTGTTGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTC  
ATGGGATCCAGAATAAATGGTGTTCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT  
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG  
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGGTATGAC  
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTA  
CAAAAATGATAGCCTATTTAAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCA  
CATATATTTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAACTTTATGTTTAAAT  
AAGAATCATTTGCTTTGAGTTTTTATATTCTTACACAAAAGAAAATACATATGCAGTCTA  
GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTCACGAGAACAACTTTGT  
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAGG  
ATAATTCTAAGTGAAATTTAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG  
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG  
GATAACAGAGAGATACCACATGACTCCAAAAAAAAAAAAAAAAA

T05T01 66282650

## **FIGURE 179**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829

><subunit 1 of 1, 436 aa, 1 stop

><MW: 49429, pI: 4.80, NX(S/T): 0

MLKVSAVLCVCAAAWCSQSLAAAAVAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR  
DEVEDDYFRTWSPGKPFQALDPAKDPCLMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA  
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCPCP  
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTKTLRPERSRFDTSILPI  
CKDSLGMFMNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ  
RQQDPPCQTELSNIQKRQGVKLLGQYIPLCEDEGYYKPTQCHGSVGQCWCVDRYGNEVMGS  
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDDEDEGDDDDGGDDHDVYI

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Leucine zipper pattern.**

amino acids 246-267

#### **N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

#### **Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352

097829-101501  
TOSTOT" 66284660



# FIGURE 180

CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGC  
 CTCTTTTCAGCCCGGGATCGCCCCAGCAGGGATCGGGCGACAAGATCTGGCTGCCCTTCCCCGTGCTCCTTCTGGCC  
 GCTCTGCCCTCCGGTGCTGCTGCCCTGGGGCGGCCGGCTTCACACCTTCCCTCGATAGCGACTTCACCTTTACCCCTT  
 CCCGCCGGCCAGAAGGAGTGCTTCTACCAGCCCATGCCCTGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTTTA  
 GATGGAGCAGGATTAGATATTGATTTCCATCTTGCCTCTCCAGAAGGCAAAACCTTAGTTTTTGAACAAAGAAAA  
 TCAGATGGAGTTTCACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACATTTCAGCACCATT  
 TCTGAGAAGGTGATTTTTCTTTGAATTAATCCTGGATAATATGGGAGAACAGGCACAAGAACAAAGAGATTGGAAG  
 AAATATATTACTGGCACAGATATATTGGATATGAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCC  
 AGACTAAGCAAAAGTGGGCACATACAAATTCTGCTTAGAGCATTTGAAGCTCGTGATCGAAACATACAAGAAAGC  
 AACTTTGATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTTCATGGTGGTGGTGTGAGCCATTCAAGTTTAT  
 ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACTTAAACTCCAACTAGAGTACGTAACATTGAAA  
 AATGAGGCATAAAATGCAATAAACTGTTACAGTCAAGACCATTAAATGGTCTTCTCCAAATATTTTGAGATATA  
 AAAGTAGGAAAACAGGTATAATTTAATGTGAAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAG  
 TTGTACTTAAGTGTGTAACAGGAATATTTTGAGAATATAGGTTAACTGAATGAAGCCATATTAATAACTGCAT  
 TTTCTTAACCTTTGAAAAATTTTGCAAAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCCTAATTGCAACACC  
 AGTCTGTTTTTAACAGGTTCTATTACCCAGAACTTTTTTGTAAATGCGGCAGTTACAAATTAACGTGGAAGTTT  
 TCAGTTTTAAGTTATAAATCACCTGAGAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAAGCCCAA  
 CTTTTCTCTATTTACATATGCATCTCTCCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTG  
 AGATTTTTATAACCAATACATTTCACTGTAAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTTGCTTACATTC  
 CCAAAAGCTGACATTTTACGATTCTTAAAAACACAAAGTTACACTTAATAAATTAGGACATGTTTTCTCTTTTG  
 AAATGAAGAATATAGTTTAAAGCTTCTCCTCCATAGGGACACATTTTCTCTAACCCCTTAACATAAGTGTTAGGA  
 TTTTAAATTAATGTGAGGTAAATAAGTTTATTTTTAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA  
 TAATCATGTTATGTTAATTTTAACATGATTGCTGACTTGGATAATTCATTATTACCAGCAGTTATGAAGGAAATA  
 TTGCTAAAATGATCTGGGCCTACCATAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTATCAGAAAACAGGAA  
 AGAATTTAGAAAACTTGAGAAAACCTAATCCAAAATAAATTCACCTAAGTAGAAGCTATAAATAAATATCTAGA  
 ATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG  
 AAACCTTTGGCTGTAGGTTTTTATTTTCTACAAGAATTCTGGTTTGAATTATTTTTGTAGCAGGTACATTTTATA  
 AAATGTAAGCCCTACTGTAAGGTTTAGCACTGGGTGTACATATTTATTAAAAATTTTTATTATAACAACTTTTTAT  
 TAAAAATGGCCTTTCTGAACACTTTATTTATTGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTTTTAAA  
 CACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTTGAAGTCTATGGGGGTCTTAC  
 TCAAGTACTAGTAATTTAACTTCATCATGAATGAACATAAATTTTAAGTTATGCCCATTTATAACGTTGTTTTAT  
 GACTACATTGTGAGTTAGAAAACAACTTAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATT  
 CTTGATGAGCAATAATGATAACCAGAGAGTGATTTTCACTTACACTCATAGTAGTATAAAAAGAGATACATTTCCC  
 TCTTAGGCCCCCTGGGAGAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAAATGCCGTAT  
 ATGATCAATTACCTTAATTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACTTGCAGAACAA  
 AGGTCAATAAGATCCTTGCCATGAATACCCCTCCCTTTTGGCTGTTAAATTTGCAATGAGAAGCAAATTTTACA  
 GTACCATAACTAATAAAGCAGGGTACAGATATAAACTACTGCATCTTTTCTATAAACTGTGATTAAGAATTCTA  
 CCTCTCCTGTATGGCTGTTACTGTACTGTACTCTCTGACTCCTTACCTAACAAATGAATTTGTTACATAATCTTCT  
 ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTGAGTAACCTTCTTACCATATAAAAACGATAATTGCTT  
 TATTTGGAAAAGAATTTAGGAATACTAAGGACAATTATTTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG  
 CATAACCAAAAAAGCAAACTTGTAACAGAGTAAAAATCTTAAATATTTCTAAAGACATACTGTTTATCTGCTT  
 CATATGCTTTTTTTAAATTTCACTATTCCATTTCTAAATTAAGTTATGCTAAATTGAGTAAGCTGTTTATCACTT  
 AACAGCTCATTTTGTCTTTTCAATATACAAATTTTAAAAATACTACAATATTTAACTAAGGCCCAACCGATTTT  
 CATAATGTAGCAGTTACCGTGTTACCTCACACTAAGGCCTAGAGTTTGCTCTGATATGCATTTGGATGATTAAT  
 GTTATGCTGTTCTTTTATGTGAATGTCAAGACATGGAGGGTGTGTTGAATTTTATGGTAAAAATTAATCCTTCTTA  
 CACATAATGGTGTCTTAAATTTGACAAAAATGAGCACTTACAATTGTATGTCTCCTCAAATGAAGATTCTTTAT  
 GTGAAATTTTAAAGACATTGATTCCGCATGTAAGGATTTTTTATCTGAAGTACAATAATGCACAATCAGTGTTG  
 CTCAAACCTGCTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATAA  
 AAATTATCAAAGGAAAA

09978299-101501

## **FIGURE 181**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26017, pI: 4.73, NX(S/T): 0

MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFITLPAGQKECFYQPMPLKASLEIEY  
QVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFFEL  
ILDNMGEQAQEQEDWKKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDN  
IQESNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 195-217

#### **N-myristoylation site.**

amino acids 43-48

#### **Tyrosine kinase phosphorylation site.**

amino acids 55-62

09978299-101501  
105101-55282660

## FIGURE 182

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT  
CTCACCAGAGAGTTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGTCTCTGGATG  
CTGCTTTCCTGCCTCATTCTCCTGTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCC  
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT  
TTTTGTCAACCAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA  
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCTGGTGAGGAGCATTAG  
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG  
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC  
TCCACCATCTTAAACCCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG  
GAAAGATTATACTGTGATGCAAAGTTACCCCTATGTCTGCAAGTTCAAGGACTAGGGGCAGGT  
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC  
TCACCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTCATGATCCTCC  
TTCTTTTTCCTTTTTCTTCACCTTCATTTTCAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC  
TCAGAGAATAATAATAAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

09978299.101501

## FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM  
DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS  
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

### **Important features:**

#### **Signal peptide:**

amino acids 1-26

#### **C-type lectin domain signature.**

amino acids 146-171

09078299.101504  
105101" 66282660

## FIGURE 184

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC  
ACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGCTGGC  
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT  
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC  
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA  
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCCTGTCCTGCTGCAATACTG  
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC  
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCCATGGCCCTATGCGGCCCA  
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

097829 10150  
FOSTOT" 66282650

## FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP

FQGDSTVTKSCASKCKPSDVDGIGQTLPVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

**Important features:**

**Signal peptide:**

amino acids 1-17

**N-glycosylation site.**

amino acids 46-49

09978293-101501  
TDSOT-55284660

# FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC  
ACGGTTTTCTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT  
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG  
TAGCGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTTCTC  
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC  
TGCAGTCAGCGCCGCGCCGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTTGACA  
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA  
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA  
GACACTTCTGGTCCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCAT  
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC  
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGA  
GACACTAAACCAGCTATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACC  
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTTAGTTAAGCAT  
TCCAATAACACCTTCCAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCCTG  
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA  
AACTTTTAATTATTTTTCTAAAGGTGCTGCACTGCCTATTTTTCTCTTGTATGTAAATTT  
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT  
TCAGCTTATAGTTCTTAAAAGCATAACCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA  
AGGATCTCTTGGAATGACAAATGATAGGTACCTAAAATGTAAACATGAAAATACTAGCTTATT  
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA  
AATAAAATTTAACATTTAAAAA

## FIGURE 187

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA  
APGILYPGGNKYQTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRKRCMRH  
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG  
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQ  
KDHHQASNSSRLHTCQRH

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 256-259

**Fungal Zn(2)-Cys(6) binuclear cluster domain**

amino acids 110-126

09070229.101501



## FIGURE 188

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCTGGACCTGATTTTGCAGCGGA  
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTTCTTTCCTTCNG  
GAGTCCTTNTGAGANGATGGTTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG  
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC  
AATTCCAACGNTATCAAGAACCTGCCCCCACCNTGGGCGGCGCTGCGGGGCACCCAGGNTT  
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCANGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTNTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGG

09078299.101501  
FOIOT 66282650

# **FIGURE 189**

GAGGAACCTACCGGTACCGGCCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATCCCGTGCGCCGCGG  
 CTGGGCCGTGCGGAGAGTGCCTGTGCTTCTCTCCTGCACGCGGTGCTTGGGCTCGGCCAGGCGGGGTCCGCCGCCA  
 GGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGACCCCGCGATGGCAAGGTATATTTTTGTGGAATGAAAAGGA  
 AGTATTAGAAATGAGCTGAAGACCATTACAGATTAATATTTTTGGGGACAGATTTGTGATGCTTGATTACCCCT  
 TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTTAC  
 TTAATCAGAACTTGCAATAAGAAAGAGAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAA  
 GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTACAGTTTACTTGG  
 AGTGTCAAAACTGCAAGCAGTAGAGAAATAAGACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCTCTGATAA  
 AAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA  
 TCTACGAAAAAAGTATGACAAATATGGAGAAAAGGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA  
 CTATTATCGTTATGATTTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGGAAAGAGAGAAATTTGATGC  
 TGCTGTAAATCTGGAGAACTGTGGTTTTGTAAATTTTTACTCCCCAGGCTGTTTCACTGCCATGATTTAGTCCC  
 CACATGGAGAGACTTTGCTAAAGAAGTGGATGGGTACTTCGAATTGGAGCTGTAACTGTGGTGATGATAGAAT  
 GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCCAGTCTCTTCATTTTTCGGTCTGGAATGGCCCCAGTGAAATA  
 TCATGGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTGCAATGCAGCATGTTAGAAGTACAGTGACAGAACTTTG  
 GACAGGAAATTTTGTCAACTCCATACAACTGCTTTTGTCTGCTGGTATTGGCTGGCTGATCACTTTTTGTCAA  
 AGGAGGAGATTGTTTTGACTTCACAGACACGACTCAGGCTTAGTGGCATGTTGTTTCTCAACTCATTTGATGCTAA  
 AGAAATATATTTGGAAGTAATACATAATCTTCAGATTTTGAACACTTTTCGGCAAAACACACTAGAGGATCGTTT  
 GGCTCATCGGTGGCTGTTATTTTTTTCATTTTGGAAAAAATGAAATTCAAATGATCCTGAGCTGAAAAAACT  
 AAAAACTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGACTGTTTCTCTGCACCAGACATCTGTAGTAA  
 TCTGTATGTTTTTTCAGCCGTCTCTAGCAGTATTTAAAGGACAAGGAACCAAAGAATATGAAATTCATCATGGAAA  
 GAAGATTCTATATGATATACTTGCCTTTGCCAAAGAAAGTGTGAATTCATGTTACCACGCTTGGACCTCAAAA  
 TTTTCTGCCAATGACAAAGAACCATGGCTTGTGATTTCTTTGCCCCCTGGTGTCACCATGTGAGCTTTTACT  
 ACCAGAGTTACGAAGAGCATCAAATCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTTATGA  
 GGGACTCTGTAACATGTATAACATTCAAGCTTATCCAAACACAGTGGTATTCAACCAGTCCAACATTCTGAGTA  
 TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTCATAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC  
 ACCCACCACCTTCAACGAAGTGTACACAAAGAAAACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTG  
 GTGTATCCTTGCAGTCTTAATGCCAGAATGGAAAAGAAATGGCCCGGACATTAAGTGGACTGATCAACGTGGG  
 CAGTATAGATTGCCAACAGTATCATTCTTTTTGTGCCCAGGAAAACGTTCAAAGATACCCTGAGATAAGATTTTT  
 TCCCCCAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGATGCTTATTTCCCTGAGAAT  
 CTGGGGTCTAGGATTTTTTACCTCAAGTATCCACAGATCTAACACCTCAGACTTTCAGTGAAAAAGTTCTACAAGG  
 GAAAAATCATTGGGTGATTGATTTCTATGCTCCTTGGTGTGGACCTTGCCAGAATTTTGTCTCAGAATTTGAGCT  
 CTTGGCTAGGATGATTAAAGGAAAAGTGAAGCTGGAAAAGTAGACTGTGAGGCTTATGCTCAGACATGCCAGAA  
 AGCTGGGATCAGGGCCTATCCAAGTGTAAAGTTTTATTTCTACGAAAAGAGCAAAGAGAAATTTTCAAGAAGAGCA  
 GATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAAAAATGGAACCTCTCCGAAATCAAGGCAA  
 GAGGAATAAGGATGAACTTTGATAATGTTGAAGATGAAGAAAAAGTTTAAAAAGAAATTTGACAGATGACATCAG  
 AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCA  
 GAATTATCTACAGCACTGGTGTAAAAGAGGGTCTGCAAACTTTTCTGTAAAGGGCCGGTTTATAAATATTTTGA  
 GACTTTGCAGGCTATAATATATGGTTTACACATGAGAACAAAGATAGAGTCATCATGTATTCTTTGTTATTTGCT  
 TTTAACAACTTTTAAAAAATATTTAAACGATTCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTGAGTCCATG  
 GACCATAGATTGCTGTCCCCCTCGACGGACTTATAATGTTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCT  
 ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTTCACGTTTTTTTGGCTGACCTGAAAAGAGGTAAT  
 TAGTTTTTGGTCACTTGTCTCTCTAAAAATGCTATCCCTAACCATATATTTATATTTTCGTTTTAAAAACACCCAT  
 GATGTGGCACAGTAAACAAACCCTGTATGCTGTATTTATGAGGAGATTCTTCATTGTTTTCTTTCTCTCTCA  
 AAGGTTGAAAAAATGCTTTTAAATTTTTCACAGCCGAGAAAACAGTGCAGCAGTATATGTGCACACAGTAAGTACAC  
 AAATTTGAGCAACAGTAAGTGCACAAATTTCTGTAGTTTGTGTATCATCCAGGAAAACCTGAGGGAAAAAATTA  
 TAGCAATTAAGTGGGCTTGTAGAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA  
 TGTGTTTATGATTTTTCTGAAATGCTTTCATAGAAATTTTCCCACTGATAGTTGATTTTTGAGGCATCTAATAT  
 TTACATATTTGCCTTCTGAACTTTGTTTTGACCTGTATCCTTTATTTACATTGGGTTTTTCTTTTATAGTTTTGG  
 TTTTTCACTCCTGTCCAGTCTATTTATTTTCAAATAGGAAAAATTAATTTTACAGGTTGTTTTTACTGTAGCTTAT  
 AATGATACGTAGTTATTTCCAGTTACTAGTTTACTGTGAGGGGCTGCCTTTTTTTCAGATAAATATTGACATAATA  
 ACTGAAGTTATTTTTTATAAGAAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTTGTAGA  
 CTCAAAGAATCACAAATTTGTGAGTAAATGATGTTGTTTGTAGTTATAAATTCAGAGTGTACAGAATGGTAAAAAT  
 CCAATCAGTCAAAGAGGTCAATGAATTAAGGCTTGCAACTTTTTTCAAAAAAAAAAAAAAAAAA

1057629.10501

## **FIGURE 190**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL  
HPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGLLEDNQGGQYESWNYRYDFGI  
YDDDPEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC  
GDDRMLCRMKGVNSYPSLFI FRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNS  
IQTAFAAGIGWLITFC SKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN  
TLEDRLAHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSPLYVFQF  
SLAVFKGQGTKEYEIHGKILYDILAFAKESVNSHVTTLGPNFPANDKEPWLVDFFAPWC  
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVFVNQSNIEYEGHHS  
AEQILEFIEDLMNPSVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART  
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG  
FLPQVSTDLTPTQTFSEKVLQGNHVIDFYAPWCGPCQNFAPFELLARMIKGKVKAGKVDC  
QAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLETLRNQGKRKDEL

### **Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 744-747

**Cytochrome c family heme-binding site signature.**

amino acids 158-163

**Nt-dnaJ domain signature.**

amino acids 77-96

**N-glycosylation site.**

amino acids 484-487

097329-101501  
TOSTOT 5625/560

## FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA  
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGA  
GTCGTTGGTGAAGTTTTTTCATTCCCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA  
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC  
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA  
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT  
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA  
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA  
CATCCTAGGACATTTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG  
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCCCTACCTCATCCCATAT  
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT  
GGGAAAAACTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTCACCA  
AAAATCCAAGCACAAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA  
GATGGAATACTTACCAATAAGAAAATGATTTTTTGTTCATCGTATATCAATATCTTTCTGAG  
ACTACAGAAGTTTCTTCCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT  
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAATAAATAAGCTCCAGCCAGAGATG  
TATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTTACATTTTT  
TCAGTCCTGATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA  
ATTACCTGTCTTCCTGTTTTCTCAAGAATATTTACGTAGTTTTTTCATAGGTCTGTTTTTCTT  
TCATGCCTCTTAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT  
TTTATTTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT  
TATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG  
AATATCAACAAGAACACAGAATGAGTGACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT  
ATCTCAACCTGGACATATTTTAAGATTTCAGCATTTGAAAGATTTCCCTAGCCTCTTCCTTTT  
TCATTAGCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT  
AACTCTGAAGTCCACCAAAAGTGGACCTCTATATTTCCCTCCCTTTTTATAGTCTTATAAGA  
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAGTTCTAGCCCCATGA  
TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAA  
TTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA  
CAATGGACCCAAGAGAAGAA

## FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI  
LVLWDINKRGVEETAAECKRLGVTAHAYVVDCSNREEIYRSLNQVKKEVGDTVIVVNNAGTV  
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC  
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFNVTGFTKNPSTRLWPVLETDEVVRSLID  
GILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

**Important features:**

**Signal peptide:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-33 and 58-61

**Short-chain alcohol dehydrogenase family protein**

amino acids 165-202, 37-49, 112-122 and 210-219

09378299.101501  
"66284560"

## FIGURE 193

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCCAGCAGG  
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCCGAGAGGGGCCAGCCCGCCCGGGG  
AGGATGACCAAGGCCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTTCGGTGTTTCATGATCCT  
GCTGATCATCGTGTAAGTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCCTTCT  
CTAGGCCGCACACGGGGCCGCGCTGCCCCACGCCCCGGGCGGACAGGGACAGGGAGCTCACG  
GCCGACTCCGATGTGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA  
CCTTCCCAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG  
GCTACGACTGGTCCCCGCGCGACGCCCCGGCGCAGCCCAGACCAGGGCCGGCAGCAGGCGGAG  
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCG  
CGCATTTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGACGACCGGCACGGGG  
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG  
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA  
CGTGACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT  
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTTCTCGTGCGCGACCCC  
TTCGTGCGCCTGATCTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG  
CAAGTTCGCCGTGCCCATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCCTCGGCGC  
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCTTCGCCAACTTCATCCAGTACCTGCTGGAC  
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA  
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC  
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG  
ACCGCCAGCAGCTGGGAGGAGGACTGGTTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT  
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC  
GAGACTGAAAGCTTTCGCGTTGCTTTTTCTCGCGTGCTTGAACCTGACGCACGCGCACTCC  
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC  
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAATATATTTTCAGGTATTTAATACGA

09078299.101501

## **FIGURE 194**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGVSVMILLIIIVYWDSAGAAHFYLHTSFSPHTGPPLPTPGPDRDRELT  
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEEVSRGYDWSPRDARRSPDQGRQQAER  
RSVLRGFCANSSLAFTPKEAFDDIPNSELHSLIVDDRHGAIYCYVPKVACTNWKRMIVLS  
GSLLRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF  
VRLISAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP  
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLEDAAQLLQLLQVDRQLRFPPSYRNRT  
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

**Important features:**

**Signal peptide:**

amino acids 1-31

**N-glycosylation sites.**

amino acids 134-137, 209-212, 280-283 and 370-373

**TNFR/NGFR family cysteine-rich region protein**

amino acids 329-332

09978299-101501  
T05T0T" 66284660

## FIGURE 195

TCGGGCCAGAATTTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA  
AAGAGGCCCAGAGTAGAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT  
ATGCCGGGAAGGTGGTGGTCGTGACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC  
GCCTTCGTGAACAGCGGGGCCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCGGGC  
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG  
TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTTGGCCGCCTGGATTGTGTTGTCAACAAC  
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT  
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA  
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA  
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA  
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG  
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG  
CCACTGGGCCCGCATGGGCCAGCCCGCTGAGGTGCGGGCTGCGGCAGTGTTCTGGCCTCCGA  
AGCCAACTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGCAGAGCTGGGGTACGGGT  
GCAAGGCCAGTCGGAGCACCCCCGTGGACGCCCCCGATATCCCTTCCTGATTTCTCTCATTT  
CTACTTGGGGCCCCCTTCCTAGGACTCTCCCACCCCAAACCTCCAACCTGTATCAGATGCAGC  
CCCCAAGCCCTTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGGTACCCTGCAGGTTCCCAT  
AAAAACGATTTGCAGCC

09978299-101501



## FIGURE 196

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVTGGGRGIGAGIVRAFVN SGARVVICDKDESGGRALEQELPGAVFILCD  
VTQEDDVKTLVSETIRRFGR LDCVVNNAGHHPPPQRPEETSAQGFRQLLELNLLGTYTLTKL  
ALPYLRKSQGNVINISSLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN  
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTGG  
AELGYGCKASRSTPVDAPDIPS

**Important features:**

**N-glycosylation site.**

amino acids 138-141

**Short-chain alcohol dehydrogenase family protein**

amino acids 10-22, 81-91, 134-171 and 176-185

09978299.101501

## FIGURE 197

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGACTGGCCTCACAACCTG  
CTGTTTCTTCTTACCATTTCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA  
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCTGGCCCCTGGCCCTCACCAGGTGCCACTGGACC  
TGGTGTCACGGATGAAACCGTATGCCCCGATGGAGGAGTATGAGAGGAACATCGAGGAGATG  
GTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT  
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCC  
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCCTGTGTCTGGGCTGTGTGAACCCCTTCACC  
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTTCAGCCAGGTTCTGTGCGCCGCCG  
CCTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG  
CTGTGGGCTGCACCTGCATCTTCTTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCGAGA  
CCATCCTCCTTGACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA  
GCAAG

09978299-101501  
TOSTOT" 65284660

## FIGURE 198

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY  
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRI PVDLPEARCLCL  
GCVNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETI AVGCTCIF

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **N-glycosylation site.**

amino acids 75-78

#### **Homologous region to IL-17**

amino acids 96-180.

09978299.101501  
"TOSTOT" 66282660

# FIGURE 199

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG  
CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCG  
GCGCCCAACATGGCGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCCTGGAT  
CGCGGCTGTGGCGGCGACGGCAGGCCCCGAGGAGGCCGCGCTGCCGCCGGAGCAGAGCCGGG  
TCCAGCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGAATGCTGAAATTT  
TACGCCCCCATGGTGTCCATCCTGCCAGCAGACTGATTCAAGAATGGGAGGCTTTTGCAAAGAA  
TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTG  
GCCGCTTCTTTGTCACTACTCTCCAGCATTTTTTTCATGCAAAGGATGGGATATTCCGCCGT  
TATCGTGGCCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC  
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC  
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACTATTTTCACAGTGACTCTTGGAATT  
CCTGCTTGGTGTCTTATGTGTTTTTCGTATAGCCACCTTGGTTTTTGGCCTTTTTTATGGG  
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC  
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG  
GAGGAAAAAGATGATTCAAATGAAGAAGAAACAAAGACAGCCTTGTAAGATGATGAAGAAGA  
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACTTGGCTG  
CTGGTGTGGATGAGGAGAGAAAGTGAGGCCAATGATCAGGGGGCCCCCAGGAGAGGACGGTGTG  
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCCAGC  
TGACACAGAGGTGGTGAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGAC  
TGTAGATTTAATGATGCGTTTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGG  
CCTGCAGTTTGTACCAAATCCTTAATTTTTTCTGAATGAGCAAGCTTCTCTTAAAGATGCT  
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT  
GACAATCAGGATATAGAAAAACAAACGTAGTGTGGGATCTGTTTGGGAGACTGGGATGGGAA  
CAAGTTCATTTACTTAGGGGTGAGAGAGTCTCGACCAGAGGAGGCCATTCCAGTCCTAATC  
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCT  
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGCATCCTTTTCTTGTGTAAAGTATTTAT  
TTTTGTCAAATTGCAGGAAACATCAGGCACCACAGTGCATGAAAAATCTTTCACAGCTAGAA  
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCAGCCCTCTGAATCTCCTG  
TGCTATGTTTTATTTCTTACCTTTAATTTTTCCAGCATTTCCACCATGGGCATTGAGGCTCT  
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC  
TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT  
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT  
TTACAAGACAGATTAAAAAAAATTGTTTTGTCCAAATATAGTTGTTGTTGATTTTTTTTT  
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCCTCTAAGTCTTGCCAGTACAAGGTAGT  
CTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTTCATCTCAAGGGGTTCCCTGGGTCTTGAAC  
TACTTTAATAATAACTAAAAAACCTTCTGATTTTTCTTTCAGTGATGTGCTTTTGGTGAAA  
GAATTAATGAACCTCAGTACCTGAAAGTGAAAGATTTGATTTTGTTCATCTTCTGTAATC  
TTCCAAAGAATTATATCTTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG  
GCTAATTTCTTT

## FIGURE 200

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAAATAAGPEEAALPPEQSRVQPMNASNWTLMEGEWMLKFYAP  
WCPSCQQTDSWEAFKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFFRYRG  
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW  
CSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSESRSEQNRRSEEAHRAEQLQDAEEEEK  
DDSNEEENKDSLVDDEEEKEDLGDEDEAEEEEEEEDNLAAGVDEERSEANDQGPPGEDGVTRE  
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **Transmembrane domain:**

amino acids 191-211

#### **N-glycosylation site.**

amino acids 46-49

#### **Thioredoxin family proteins.** (homologous region to disulfide isomerase)

amino acids 56-72

#### **Flavodoxin proteins**

amino acids 173-187

09978299 "101501  
T05T01" 66282660

# FIGURE 201

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCCACATGATT  
TGA CTCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAAGAAAAGAGCTCC  
CAAATGCTATATCTATTTCAGGGGCTCTCAAGAACAAATGGAATATCATCCTGATTTAGAAAAAT  
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT  
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG  
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCTGGGTACCATGGGGGTCTTTTCC  
AGCCCTTGTCCTCCTAATTGGATTATATATGAGAAAGAGCTGTTATCTATTTCAGCATGTCACT  
AAATTCCTGGGATGGAAGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG  
ACAGCTCAAATGAATTGGGATTTATAGTAAAACAAAGTGTCTTCCCAACCTGATAATTCATTT  
TGGATAGGCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT  
CTCTTCTAACTTATTTTCAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCAAATTGTG  
TATGGATTACGTGTGAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT  
GAGAAGAAGTTTTCAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA  
AGGAGGACAGAAAAACAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATG  
TTTAGAGAGCTTGGCCAACTGTAATCTTAACCAAGAAATTGAAGGGAGAGGCTGTGATTTCT  
GTATTTGTGCGACCTACAGGTAGGCTAGTATTATTTTTCTAGTTAGTAGATCCCTAGACATGG  
AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTATTTTATTTTGGAGATAGGGTCT  
CACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC  
CTCAGCCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTGGTG  
TTTTTTGTAGAGACTGGGTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG  
TGATCTGCCCCGCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC  
CCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTACCTTGGGTAAGCCATAAGCGA  
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTTCATGCTCAACAATGCCATTGAAGTGCACGGT  
GTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAAT  
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTT  
ATTATTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACCTCCTA  
CTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT  
TTTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTGCAACGG  
CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCT  
CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTTAGT  
AGAGACAGGGTTTCTCCATGTGCGTTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC  
CTGCCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT  
TGTATAATATGTAATTGTAGGGAAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTTAAATACA  
AAAATACATAAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA  
ACAAGTATTAACATTTTGGAAATATGTTTTATTAGTTTTTGTGATGTACTGTTTTACAATTTTT  
ACCATTTTTTTTCAGTAATTACTGTAAAATGGTATTATTGGAATGAACTATATTTCTCATG  
TGCTGATTTGTCTTATTTTTTTTCATACTTTCCCACTGGTGCTATTTTTTATTTCCAATGGATA  
TTTCTGTATTACTAGGGAGGCATTTACAGTCCTCTAATGTTGATTAATATGTGAAAAGAAAT  
TGTACCAATTTTACTAAATTATGCAGTTTAAAATGGATGATTTTATGTTATGTGGATTTTCAT  
TTCAATAAAAAAAACTCTTATCAAAAAA

09978299 " 101501

## FIGURE 202

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLLIAVILGILCLVILVIAV  
VLGTMGVLSSPCPPNWIIYEKSCYLFSMSLNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ  
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL  
CSVPSYSICEKKFSM

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 45-65

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 197-200

#### **N-myristoylation sites.**

amino acids 35-40 and 151-156

#### **Homologous region to LDL receptor**

amino acids 34-67 and 70-200.

09978299 101501  
T05T0T 66282660

# FIGURE 203

GGAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCAGACCTGGAGGGTCTCGCTCTGTCA  
 CACAGGCTGGAGTGAGTGGTGTGATCTTGGCTCATCGTAACCTCCACCTCCCGGGTTCAAGTGATTCTCATGCC  
 TCAGCCTCCCGAGTAGCTGGGATTACAGGTGGTGACTTCCAAGAGTGACTCCGTGCGAGGAAAATGACTCCCCAG  
 TCGCTGCTGCAGACGACACTGTTCTCTGCTGAGTCTGCTCTTCTGGTCCAAGGTGCCCACGGCAGGGGCCACAGG  
 GAAGACTTTTCGCTTCTGCAGCCAGCGGAACCAGACACACAGGAGCAGCCTCCACTACAAACCCACACCAGACCTG  
 CGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCCCTTCCCTGCAGCCCACCCTGCTTCCCGA  
 TCCTTCCCTGACCCAGGGGCTCTACCACTTCTGCCTCTACTGGAACCGACATGCTGGGAGATTACATCTTCTC  
 TATGGCAAGCGTGACTTCTTGTGCTGAGTGACAAAGCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGCCTG  
 GCTCAGGGCCCCCGCTGTAGCCACTTCTGTACCTCCTGGTGGAGCCCTCAGAACATCAGCCTGCCAGTGCC  
 GCCAGCTTCACTTCTCTTCCACAGTCTCCCCACACGGCCGCTCACAATGCCTCGGTGGACATGTGCGAGCTC  
 AAAAGGGACCTCCAGCTGCTCAGCCAGTTCCTGAAGCATCCCCAGAAGGCCTCAAGGAGGCCCTCGGCTGCCCCC  
 GCCAGCCAGCAGTTGCGAGCCTGGAGTCGAAACTGACCTCTGTGAGATTATGGGGGACATGGTGTCTTTCGAG  
 GAGGACCGGATCAACGCCACGGTGTGGAAGCTCCAGCCACAGCCGGCCTCCAGGACCTGCACATCCACTCCCCG  
 CAGGAGGAGGACAGAGCCGAGATCATGGAGTACTCGGTGCTGCTGCCTCGAACACTCTTCCAGAGGACGAAAGGC  
 CGGAGCGGGGAGGCTGAGAAGAGACTCCTCCTGGTGGACTTCAGCAGCCAAGCCTGTTCCAGGACAAGAATTCC  
 AGCCAAGTCTGGGTGAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAAGTAGCCAACCTCACGGAGCCCGTG  
 GTGCTCACTTTCAGCACCAGCTACAGCCGAAGAATGTGACTCTGCAATGTGTGTTCTGGGTGAAGACCCACA  
 TTGAGCAGCCCGGGCATTGGAGCAGTGTGGGTGTGAGACCGTCAGGAGAGAAACCCAAACATCTGCTTCTGC  
 AACCATTGACCTACTTTGCACTGCTGATGGTCTCTCGGTGGAGGTGGACGCCGTGCACAAGCACTACCTGAGC  
 CTCCTCTCTACGTGGGCTGTGCTGCTCTGCCCCGGCTGCTTGTACCATTGGCCGCTACCTCTGCTCCAGG  
 GTGCCCTGCGGTGCAGGAGGAAACCTCGGGACTACACCATCAAGGTGCACATGAACCTGCTGCTGGCCGTCTTC  
 CTGCTGGACACGAGCTTCTGCTCAGCGAGCCGGTGGCCCTGACAGGCTCTGAGGCTGGCTGCCGAGCCAGTGCC  
 ATCTTCTGCACTTCTCTCTGCTCACTGCTCTTCTGGATGGGCCTCGAGGGGTACAACCTCTACCGACTCGTG  
 GTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTT  
 CTGGTGACGCTGGTGGCCCTGGTGGATGTGGACAACATATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAG  
 GCGCTCATCTACCTTCCATGTGCTGGATCCGGGACTCCCTGGTCACTACATCACCACCTGGGCCTCTTCAGC  
 CTGGTGTCTGTCTCAACATGGCCATGCTAGCCACCATGGTGGTGCAGATCCTGCGGCTGCGCCCCCACACCCAA  
 AAGTGGTCACATGTGCTGACACTGCTGGGCCTCAGCCTGGTCTTGGCCTGCCCTGGGCCTTGATCTTCTTCTCC  
 TTTGCTTCTGGCACCTTCCAGCTTGTGCTCTCTACCTTTTCAGCATCATCACCTCTTCCAAGGCTTCTCTCATC  
 TTCACTGGTACTGGTCCATGCGGCTGCAGGCCCGGGTGGCCCTCCCCCTGTAAGAGCAACTCAGACAGCGCC  
 AGGCTCCCCATCAGCTCGGGCAGCACCTCGTCCAGCCGCATCTAGGCCTCCAGCCACCTGCCCATGTGATGAAG  
 CAGAGATGCGGCCTCGTCGACACTGCCTGTGGCCCCGAGCCAGGCCAGCCCCAGGCCAGTCAAGCCGAGACT  
 TTGAAAGCCCCAACGACCATGGAGAGATGGGCCGTTGCCATGGTGGACGACTCCCGGGCTGGGCTTTTGAATTG  
 GCCTTGGGGACTACTCGGCTCTCACTCAGCTCCACGGGACTCAGAAGTGCGCCGCCATGCTGCCTAGGGTACTG  
 TCCCCACATCTGTCCCAACCCAGCTGGAGGCCTGGTCTCTCTTACAACCCCTGGGCCAGCCCTCATTTGCTGGG  
 GGCCAGGCCTTGGATCTTGGGGTCTGGCACATCCTTAATCCTGTGCCCCCTGCCCTGGGACAGAAATGTGGCTCCA  
 GTTGCTCTGTCTCTGCTGGTCAACCTGAGGGCACTCTGCATCCTCTGTCACTTTAACCTCAGGTGGCAGCCAGGG  
 CGAATGGGGCCAGGGCAGACCTTCAGGGCCAGAGCCCTGGCGGAGGAGAGGCCCTTTGCCAGGAGCACAGCAGC  
 AGCTCGCCTACCTCTGAGCCCAGGCCCTCTCTCTCTCAGCCCCCAGTCTCTCTCTCATCTTCTCTGGGGTTC  
 TCCTCTCTCTCCAGGGCCTCTTGTCTCTTCTGTTACAGCTGGGGGTCCCCGATTCCAATGCTGTTTTTTGGGGA  
 GTGGTTTCCAGGAGCTGCTGGTGTCTGTGTAAATGTTTGTCTACTGCACAAGCCTCGGCTGCCCTGAGCCA  
 GGCTCGGTACCGATGCGTGGGCTGGGCTAGGTCCCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATTGCCCTTG  
 CTCACCTGACCAAGCACACGCTCAGAGGGGCCCTCAGCCTCTCTGAAGCCCTCTTGTGGCAAGAACTGTGGA  
 CCATGCCAGTCCCGTCTGGTTTCCATCCCACTCCAAGGACTGAGACTGACCTCTCTGGTGACACTGGCCTA  
 GAGCCTGACACTCTCCTAAGAGGTTCTCTCAAGCCCCCAAATAGCTCCAGGCGCCCTCGGCCGCCATCATGGT  
 TAATTCTGTCCAACAAACACACGGGTAGATTGCTGGCCTGTTGTAGGTGGTAGGACACAGATGACCGACCTG  
 GTCACCTCTCTGCCAACATTCAGTCTGGTATGTGAGGCGTGCGTGAAGCAAGAACTCTGGAGCTACAGGGACA  
 GGGAGCCATCATCTCTGCTGGGAATCCTGGAAGACTTCTGTCAGGAGTCAGCGTTCAATCTTGACCTTGAAGAT  
 GGGAGGATGTTCTTTTACGTACCAATCTTTTGTCTTTTGTATATTAAGAAAGTACATGTTTATTGTAGAGA  
 ATTTGGAAACTGTAGAAGAGAATCAAGAAGAAAAATAAAATCAGCTGTTGTAATCGCTAGCAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA



## FIGURE 204

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLLQTTLFLLSLLFLVQGAHGRGHREDFRCSQRNQTHRSSLHYKPTPDLRISIENSE  
EALT VHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH  
QEESLAQGPPLLATSVTSWWSPQNISLPSAASFTHSFHSPHTAAHNASVDMCELKRDLQLL  
SQFLKHPQKASRRPSAAPASQQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD  
LHIHSRQEEEQSEIMEYSVLLPRTLFRQTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE  
KVLGIVVQNTKVANLTEPVVLTFFQHQLQPKNVTLQCVFWVEDPTLSSPGHWSSAGCETVRRE  
TQTSCFCNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVVSAACLVITIAAYLCSRVPPLPC  
RRKPRDYTIKVHNMNLLAVFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE  
GYNLYRLVVEVFVGTYPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY  
PSMCWIRDSLVSYITNLGLFSLVFLFNMA MLATMVVQILRLRPHTQKWSHVLTLGLSLVLG  
LPWALIFFSFASGTFQLVVLYLFSIITSFQGFIFIWYSMRLQARGGPSPLKSNSDSARLP  
ISSGSTSSSRI

### Important features:

#### Signal peptide:

amino acids 1-25

#### Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657

#### Microbodies C-terminal targeting signal.

amino acids 691-693

#### cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

#### N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344

#### G-protein coupled receptors family 2 proteins

amino acids 475-504

0978299.10503  
TOSTOT 66284650

## FIGURE 205

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA  
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG  
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA  
GCCAGTGCCATCTTCCTGCACCTTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG  
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA  
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG  
TGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCT  
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT  
GGTGTTTCTGTTCAACATGG

09978299-101501  
"F05T0T" 66282660

# FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTTCAGGTCCAGGTTTTGCTTTGA  
 TCCTTTTCAAAAACTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAACCTACCCT  
 GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAAGAGAC  
 TCGGGAGTCGCTGCTTCCAAAGTGCCCGCCGTGAGTGAGCTCTCACCCAGTGCAGCCAAATGAGCCTCTTCGGGC  
 TTCTCCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTCC  
 AGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG  
 GAAGTATTCACAGCCCAAGGTTTTCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG  
 AGGAAAATGTATGGATACAACCTTACGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT  
 ATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAACATATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAG  
 GAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAACCAGGGT  
 TCTGCACTCCACTACAACATTGTTCATGCCACAATTCACAGAAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTT  
 TGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAG  
 AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAAGTTGGCAACTTCTTGGCAAGGCTTTTGTTTTGGAA  
 GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTCT  
 CAGTGTCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTG  
 GTGGGAACTGTGCTGTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC  
 ACGAGGTCTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTACCGACGTGGCCCTGGAGC  
 ACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCA  
 GAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGTCT  
 TCAAGGACCTTTTCATCTTCAGGATTTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCA  
 ACAGCTCTTTTGTAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTAT  
 TAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTTCAGTTCTTTT  
 GATACGGCTTAGGGTAATGTGAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAAC  
 TCTAAAGCTCCATGTCTGGGCCTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTGTCTCATATTCACAT  
 ATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAATTAACTTGT  
 GTCATGCTGATAGGACAGACTGGATTTTTTCATATTTCTTATTTAAATTTCTGCCATTTAGAAGAAGAGAACTACA  
 TTCATGGTTTGAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACCTTTATCGATAAGTCAGTTTATTTG  
 TTTTCATTGTGTACATTTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTAAATATATCT  
 ATTTTTACCAAAGGTATTTAATATTCTTTTTTATGACAACCTTAGATCAACTATTTTTTAGCTTGGTAAATTTTTCT  
 AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCA  
 TTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAA  
 GACTTTTTTGAATAAATTAAATTATCATATCTTCCATTCTGTTATTGGAGATGAAAATAAAAAAGCAACTTATGA  
 AAGTAGACATTTCAGATCCAGCCATTACTAACCTATTCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACAT  
 AAAGCACCTTGAAGAAAGACTTGGCAGCTTCTGATAAAGCGTGTGTGCTGTGCAGTAGGAACACATCCTATTTA  
 TTGTGATGTTGTGGTTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAATACATGGATATTTTTATGTACA  
 GAAGTATGTCTCTTAACCAGTTCACTTATTGTACTCTGGCAATTTAAAAAGAAAATCAGTAAATATTTTGTCTGT  
 AAAATGCTTAATATNGTGCCTAGGTTATGTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAAAATAAAGA  
 ATGTGGCTATTTTGGGGAGAAAATTAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

105701 " 66287650

## FIGURE 207

MSLFGLLLLSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR  
FPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC  
GSGTVPKGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL  
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLY  
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQ  
LRPKTGVRGLHKS LTDVALEHHEECDVCVRGSTGG

**Signal sequence:**

amino acids 1-14

09978299-101504  
"FOST" 66282660

# FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCATTTTGAAGA  
 AGACTAAAAATGGTGTTCCTCAATGTGGACACTGAAGAGACAAATTCCTATCCTTTTAAACATAATCCTAATTTCC  
 AAACCTCTTGGGGCTAGATGGTTTCTTAAACCTCTGCCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG  
 ATCGTGGACTGCACAGACAAGCATTTGACAGAAATTCCTGGAGGTATTTCCACGAACACCACGAACCTCACCTC  
 ACCATTAAACCACATACCAGACATCTCCCAGCGTCTTTACAGACTGGACCATCTGGTAGAGATCGATTTTCA  
 TGCAACTGTGTACCTATTTCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAGC  
 TTTAGTGGACTCACTTATTTAAAAATCCCTTTACCTGGATGGAAACCAGCTACTAGAGATACCGCAGGGCCTCCCG  
 CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACACATCTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCC  
 AACATAGAAATACTCTACCTGGGCCAAAACTGTATTTATCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAA  
 GATGCCCTTCTTAACTTGACAAAGTTAAAAGTGCTCTCCCTGAAAGATAACAATGTACAGCCGTCCCTACTGTT  
 TTGCCATCTACTTTTAAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCAAGAAGATGATTTTAATAAC  
 CTCAACCAATTACAAATTTCTTGACCTAAGTGGAAATTTGCCCTCGTTGTTATAATGCCCCATTTCTTGTGCGCCG  
 TGTAAAAATAATTTCTCCCTACAGATCCCTGTAAATGCTTTTGATGCGCTGACAGAATTTAAAGTTTTACGTCTA  
 CACAGTAACCTCTCTTCAGCATGTGCCCAAGATGGTTAAGAACATCAACAACTCCAGGAACCTGGATCTGTCC  
 CAAAACCTCTTGGCCAAAGAAATTTGGGGATGCTAAATTTCTGCATTTTCTCCCCAGCCTCATCCAATTGGATCTG  
 TCTTTCAATTTTGAACCTCAGGTCTATCGTGCATCTATGAATCTATCACAAGCATTTTCTTCACTGAAAAGCCTG  
 AAAATCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA  
 AATCTTGAAGTTCTTGATCTTGGCACTAACTTTATAAAAAATTGCTAACCTCAGCATGTTTAAACAATTTAAAGA  
 CTGAAAGCTCATAGATCTTTTCACTGAATAAAATACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAAT  
 GCCAGAACCTCTGTAGAAAAGTTATGAACCCAGGTCTTGGAAACAATTACATTATTTTCAATATGATAAGTATGCA  
 AGGAGTTGCAGATTCAAAAAACAAGAGGCTTCTTTTATGTCTGTAAATGAAAGCTGCTACAAGTATGGGCAGACC  
 TTGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCCTCTGATTTTTCAGCATCTTTCTTCTCAAATGCCTG  
 AATCTGTGAGAAATCTCATTAGCCAACTCTTAATGGCAGTGAATTTCAACCTTTAGCAGAGCTGAGATATTTG  
 GACTTCTCCAACAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAGAGCTTCAAACTGGAAGTTCTGGAT  
 ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAAACTTTACCAAGAACCCTAAAGGTT  
 CTGCAGAACTGATGATGAACGACAATGACATCTCTTCTCCACCAGCAGGACCATGGAGAGTGAGTCTCTTAGA  
 ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAG  
 AATCTGTAAAAATTAGAGGAATTAGACATCTCTAAAAATTCCTAAGTTTCTTGCCTTCTGGAGTTTTTGATGGT  
 ATGCCCTCAAATCTAAAGAATCTCTCTTTGGCCAAAAATGGGCTCAAATCTTTTCAAGTTGGAAGAACTCCAGTGT  
 CTAAAGAACCCTGGAAACTTTGGACCTCAGCCACAACCACTGACCACTGTCCCTGAGAGATTATCCAACCTGTTCC  
 AGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTTCTACAAGATGCCTTC  
 CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAAGACCAGCTTCCCAGAAAATGTCCTC  
 AACAATCTGAAGATGTTGCTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTTGTCTGGTGG  
 GTTAACCATACGGAGGTGACTATTCCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGC  
 CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA  
 TCTGTATCTCTTTCTCATGGTGTGATGACAGCAAGTCACTCTATTTCTGGGATGTGTGGTATATTTTACCAT  
 TTCTGTAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTAT  
 GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAAGAGAGAAA  
 CATTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTTCCCAGAGCATA  
 CAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAAGACTGAAAATTTTAAAGATAGCATTTTAC  
 TTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTTCAAGAG  
 TCCAAGTTCTTCCAGCTCCGGAAGGGCTCTGTGGGAGTTCTGTCTTGGAGTGGCCAACAACCCGCAAGCTCAC  
 CCATACTTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGAA  
 ACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCCTGGC

10501 6628650

## FIGURE 209

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPMNHVIVDCTDKHLTEIPGG  
IPTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRNCNCPVPIPLGSKNNMCIKRLQIKPRSFS  
GLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLQNCYYR  
NPCYVVSYSIEKDAFLNLTKLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNL  
NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRRLHSNSLQHVPPRWF  
KNINKLQELDLSONFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSL  
KILRIRGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS  
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQ  
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH  
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVQLKMMNDNDISSSTSRTMESES  
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNLSFLPSGVFDGMPPNLKNLSL  
AKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQ  
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCAVWFVWVWNHTEVTIP  
YLATDVTVCVGPAGAHKGQSVISLDLYTCELDLTNLILFSLISISVSLFLMVMMTASHLYFWDVW  
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLEE  
RDWLPGQPVLENLSQSIQLSKKTVMFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVIILIFLE  
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

### Signal sequence:

amino acids 1-26

### Transmembrane domain:

amino acids 840-860

# FIGURE 210

GGGTACCATTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACAACAGAAACATGGAAAAATGTTTCCTTC  
 AGTCGTCAATGCTGACCTGCATTTTCTGCTAATATCTGGTTTCTGTGAGTTATGCGCCGAAGAAAAATTTTCTA  
 GAAGCTATCCTTGTGATGAGAAAAAGCAAAATGACTCAGTTATTGCAGAGTGCAGCAATCGTCGACTACAGGAAG  
 TTCCCCAAACGGTGGGCAAAATATGTGACAGAACTAGACCTGTCTGATAATTTTCATCACACACATAACGAATGAAT  
 CATTTCAGGGCTGCAAAATCTCACTAAAATAAATCTAAACCACAACCCCAATGTACAGCACCAGAACCGGAAATC  
 CCGGTATACAAATCAAATGGCTTGAATATCACAGACGGGGCATTCCTCAACCTAAAAAACCTAAGGGGAGTTACTGC  
 TTGAAGACAACCAGTTACCCCAAAATACCCTCTGGTTTGCCAGAGTCTTTGACAGAACTTAGTCTAATTTCAAACA  
 ATATATACAACATAACTAAAGAGGGCATTTCAAGACTTATAAACTTGAAAAATCTCTATTTGGCCTGGAACCTGCT  
 ATTTTAAACAAAGTTTGGCAGAAAACTAACATAGAAGATGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTAT  
 CACTATCTTTCAATTTCTTTTACACGTGCCACCCAACTGCCAAGCTCCCTACGCAAACTTTTTCTGAGCAACA  
 CCCAGATCAAATACATTAGTGAAGAAGATTTCAAGGGATTGATAAATTTAACATTACTAGATTTAAGCGGGAACCT  
 GTCCGAGGTGCTTCAATGCCCCATTTCCATGCGTGCTTGTGATGGTGGTGCCTTCAATTAATATAGATCGTTTTG  
 CTTTTCAAACTTGACCCAACTTCGATACCTAAACCTCTCTAGCACTTCCCTCAGGAAGATTAATGCTGCTGGT  
 TTAAAAATATGCCTCATCTGAAGGTGCTGGATCTTGAATTCAACTATTTAGTGGGAGAAAATAGTCTCTGGGGCAT  
 TTTTAAACGATGCTGCCCCGCTTAGAAATACTTGACTTGTCTTTTAACTATATAAAGGGGAGTTATCCACAGCATA  
 TTAATATTTCCAGAACTTCTCTAACTTTTGTCTCTACGGGCATTGCATTTAAGAGGTTATGTGTTCCAGGAAC  
 TCAGAGAAGATGATTTCCAGCCCCCTGATGCAGCTTCCAACTTATCGACTATCAACTTGGGTATTAATTTTATTA  
 AGCAAAATCGATTTCAAACCTTTTCAAATTTTCTCCTAATCTGGAATTAATTTACTTGTGAGAAAAACAGAAATATCAC  
 CGTTGGTAAAGATACCCGGCAGAGTTATGCAATAGTTTCTCTTTTCAACGTATATCCGGAACAGCGCTCAA  
 CAGATTTTGAGTTTGACCCACATTCGAACCTTTTATCATTTTCAACCGTCCCTTAAATAAGCCACAATGTGCTGCTT  
 ATGAAAAAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCAATGGGCCAAACCAATTTGAAAAATCTTCTGACA  
 TTGCTGTTTAAATCTGTCTGCAATAGCAATGCTCAAGTGTAAAGTGAACCTGAATTTTCAAGCATTCTCTCATG  
 TCAAAATATTTGGATTTGACAAACAATAGACTAGACTTTGATAATGCTAGTGTCTTACTGAATTTGCTCCGACTTGG  
 AAGTCTAGATCTCAGCTATAATTCACACTATTTTCAAGATAGCAGGCGTAACACATCATCTAGAATTTATTTCAA  
 ATTTTCAAAATCTAAAGTTTAAACTTTGAGCCACAACAACATTTTATACCTTTAACAGATAAGTATAACCTGGAAA  
 GCAAGTCCCTGGTAGAATTAGTTTTAGTGGCAATCGCCTTGACATTTTGTGGAATGATGATGACAAACAGGTATA  
 TCTCCATTTTCAAAGGTCTCAAGAATCTGACACGTCTGGATTTATCCCTTAATAGGCTGAAGCACATCCCAAATG  
 AAGCATTCCTTAATTTGCCAGCGAGTCTCACTGAACATACATATAAATGATAATATGTTAAAGTTTTTTAACTGGA  
 CATTACTCCAGCAGTTTCTCGTCTCGAGTTGCTTGACTTACGTGGAAACAACTACTCTTTTAACTGATAGCC  
 TATCTGACTTTTACATCTTCCCTTCGGCACTGCTGCTGAGTACATAACAGGATTTCCACCTACCCTCTGGCTTTC  
 TTTCTGAAGTCAGTAGTCTGAAGCACCTCGATTTAAGTTTCAATCTGCTAAAAACAATCAACAAATCCGCACTTG  
 AAATAAGACCACCACCAAAATTATCTATGTTGGAACCTACACGGAAACCCCTTTGAATGCACCTGTGACATTGGAG  
 ATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAATTTCCAGACTGGTAGATGTCAATTTGTGCCAGTCTCTG  
 GGGATCAAAGAGGGAAGAGTATTGTGAGTCTGGAGCTAACAACTTGTGTTTCAAGATGTCACTGCAGTGATATTAT  
 TTTCTTCAAGTCTTTTATCACCACCATGGTTATGTTGGCTGCCCTGGCTCACCATTGTGTTTACTGGGATGTTT  
 GGTTTATATATAATGTGTTTATAGTTAAGGTAAAGGCTACAGGTCTCTTTCCACATCCCAACTCTTTCTATGATG  
 CTTACATTTCTTATGACACCAAGATGCCTCTGTTACTGACTGGGTGATAAATGAGCTGCGCTACCACCTTGAAG  
 AGAGCCGAGACAAAAACGTTTCTCTTTGTCTAGAGGAGAGGGATTGGGACCCGGGATTGGCCATCATCGACAACC  
 TCATGCAGAGCATCAACCAAAGCAAGAAAACAGTATTTGTTTAAACCAAAAAATATGCAAAAAGCTGGAACCTTA  
 AAACAGCTTTTTTACTTGGCTTTGCAGAGGCTAATGGATGAGAACATGGATGTGATTATATTTATCTCTGCTGGAGC  
 CAGTGTTACAGCATTCTCAGTATTTGAGGCTACGGCAGCGGATCTGTAAGAGCTCCATCTCCAGTGGCCTGACA  
 ACCCGAAGGCAGAAGGCTTGTGTTTGGCAAACCTCTGAGAAATGTGGTCTTGACTGAAAAATGATTACCGGTATAACA  
 ATATGTATGTGATTCATTAAAGCAATACAACTGACGTTAAGTCATGATTTGCGGCCATAATAAAGATGCAAG  
 GAATGACATTTCTGTATTAGTTATCTATTGCTATGTAACAAATATCCCAAACTTAGTGGTTTAAACAACACA  
 TTTGCTGGCCACAGTTTTTGGGGTCCAGGATCCAGGCCAGCAAACTGGGTCTCTGCTCAGGGTGTCTCAG  
 AGGCTGCAATGTAGGTGTTTACCAGAGACATAGGCATCACTGGGGTCACTCATGTGGTTGTTTTCTGGATTCA  
 ATTCCTCTGGGCTATTGGCCAAAGGCTATACTCATGTAAGCCATGCGAGCCTCTCCACAAGGCAGCTTGCTTC  
 ATCAGAGCTAGCAAAAAGAGAGGTTGCTAGCAAGATGAAGTCACAATCTTTTGAATCGAATCAAAAAAGTGAT  
 ATCTCATCACTTTGGCCATATTCTATTTGTTAGAAGTAAACCACAGGTCCACCAGCTCCATGGGAGTGACCACC  
 TCAGTCCAGGGAAAACAGCTGAAGACCAAGATGGTGAGCTCTGATTGCTTCAGTTGGTTCATCAACTATTTTCCCT  
 TGACTGCTGTCTGGGATGGCCTGCTATCTTGATGATAGATTGTGAATATCAGGAGGCAGGGATCACTGTGGACC  
 ATCTTAGCAGTTGACCTAACACATCTCTTTTCAATATCTAAGAACTTTTGCCACTGTGACTAATGGTCTTAATA  
 TTAAGCTGTTGTTTATATTTATCATATCTATGGCTACATGGTTATATTATGCTGTGGTTGCGTTTCGGTTTAT  
 TTACAGTTGCTTTTACAAATATTTGCTGTAACATTTGACTTCAAGGTTTAGATGCCATTTAAGAACTGAGATGG  
 ATAGCTTTTAAAGCATCTTTTACTTCTTACCATTTTAAAGATATGCAGCTAAATTCGAAGCTTTTGGTCTATA  
 TTGTTAATTGCCATTGCTGTAAATCTTAAATGAATGAATAAAAAATGTTTCATTTTACAAAAA

09576299 " 101501

## FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQNDSVIAECSNRRLQEVPTVG  
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFLNL  
KNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV  
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEEDFKGLINL  
TLLDLSGNCPRCFNAPFPCVPCDGGASINIDRFAFQNLTLQLRYLNLSSTSLRKINAAWFKNM  
PHLKVLDLEFNVLVGEIVSGAFLTMLPRLEILDLSFNYIKGSYPQHINISRNFSKLLSLRAL  
HLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNFNLEIIYLSENRISPLV  
KDTRQSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI  
GPNQFENLPDIACNLNSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDLEV  
LDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL  
DILWNDDDNRYISIFKGLKNLTRLDLNRLKHIPNEAFLNLPASLTELHINDNMLKFFNWT  
LLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRTLTLSSHNRISHLPSGFLSEVSSLKHLDL  
SNLLKTINKSALETKTTTKLSMLELHGPNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP  
GDQRGKSIVSLELTTCVSDVTAVILFFFTFFITTMVMLAALAHHLFYWDVWFIYNVCLAKVK  
GYRSLSTSQTIFYDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWDPLAIIID  
NLMQSINQSKKTVFVLTKKYAKSWNFKTA FYLALQRLMDENMDVIIIFILLEPVLQHSQYLRL  
RQRICKSSILQWPDNPKAEGLEFWQTLRNVVLTENDSRYNMYVDSIKQY

### **Signal sequence:**

amino acids 1-26

### **Transmembrane domain:**

amino acids 826-848

09978299.101501



## FIGURE 212

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT  
 CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
 CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC  
 AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC  
 TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA  
 GCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA  
 GGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT  
 CTGGTGTTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT  
 CCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCA  
 CCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC  
 CGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGAC  
 CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGA  
 GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA  
 GATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCCGG  
 CAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC  
 CCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAA  
 GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGC  
 CCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCGGCAGCCTCC  
 TGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCTCTG  
 GAGGAGCAGCTGGGGTCTCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTG  
 GACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTCCAG  
 AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCTCCTCCCC  
 TTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC  
 CCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG  
 AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG  
 GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAATGAAACGTGA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGT  
 CGACCTGCAGAAGCTTGGCCGCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAAT

097829 10501

## FIGURE 213

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPGGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19

04978299-1050  
FOSTOT-66284650

## FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG  
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC  
AGCAGCATCAGAGCAGCCCCCTGTGGTTGGCAGCAAAGTTCAGCTTGGCTGGGCCCCGCTGTGA  
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGGCTGAGGTCTCCTCATCTTCTCCCTAGC  
AGTGGATGAGCAACCCAACGGGGGCCCCGGGGAGGGGAACTGGCCCCGAGGGAGAGGAACCCC  
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG  
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCT  
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCCGCTGGAGGCACAGGCCATGAGGGGC  
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA  
CCGGCCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCCG  
TGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC  
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA  
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT  
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA  
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTG  
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCC  
TGCTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG  
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT  
GGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC  
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGAC  
TCCCTGAGCGAGCAGATTTCTTCTCCTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGA  
CTCGTGACTGCCCAGCGCTCCAGGCTGGACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATG  
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC  
AGGGCCTTCCTCCTCTTCTCCTCCTCCCTTCTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT  
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA  
TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC  
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC  
CCCCAGCACAATAAAAATGAAACGTG

09070299-101501

## FIGURE 215

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDVSESVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSDGTLCVPKGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKDS

**Signal sequence:**

1-19

09978299-101501  
TOSTOT" 66284560

## FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA  
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG  
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT  
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC  
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC  
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGC  
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACG  
GGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGAC  
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG  
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC  
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG  
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA  
ATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT  
GCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG  
CCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG  
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACA  
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCC  
TTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCCTGGAGGAGCAGCT  
GGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGGCTGGACTGAGCCCC  
TCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG  
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCCCTTCCTCGGGAG  
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC  
CCCACCCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC  
GAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG  
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAATGAAACGTG

09978299.10501

## FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCQSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSDGTLCVPKGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19

09978299 "105101" 66282650

# FIGURE 218

GGTTGCCACAGCTGGTTTATAGGGCCCCGACCACTGGGGCCCCCTTGTCTAGGAGGAGACAGCCTCCCGGCCCGGGGAG  
 GACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTCCGTTTCTGCGCTCAGCTGCCGGCCG  
 AGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTCTGGTCTCCCTTCTCCCGCTGGGCCGGTTTATCGGGAGG  
 AGATTGTCTTCCAGGGCTAGCAATTGGACTTTTGTATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGAT  
 TTCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTCGTGAATCGCAAAACCCATTTTGGAGCAGGAATTCCAATCA  
TGTCTGTGATGGTGGTGAGAAAGAGGTGACACGAAATGGGAGAAACTCCAGGCAGGAACACCTTTTGTCTGTG  
 ATGGCCGCGTCATGATGGCCCCGGCAAAAGGGCATTTTCTACCTGACCCCTTTTCTCATCCTGGGGACATGTACAC  
 TCTTCTTCGCTTTGAGTGCCGCTACCTGGCTGTTTCTGCTGCTCCTGCCATCCCTGTATTTGCTGCCATGCTCT  
 TCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTCAGTGACCCCTGGAGTGATTCTCGGGCGCTACCAGATG  
 AAGCAGCTTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACCACCGCCTCGTA  
 TCAAGAATTTCCAGATAAACAACCAGATTGTGAAACTGAAATACTGTTACACATGCAAGATCTTCCGGCCTCCCC  
 GGGCCTCCCATTCAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCCCTGGGTGGGGAATTGTG  
 TTGGAAGAGGAACTACCGCTACTTCTACCTCTTCATCCTTTCTCTCTCCCTCCTCACAATCTATGTCTTCGCCT  
 TCAACATCGTCTATGTTGGCCCTCAAATCTTTGAAAATGGCTTCTTGGAGACATTGAAAGAAACTCCTGGAATG  
 TTCTAGAAGTCTTCTATTGCTTCTTTACACTCTGGTCCGTGCTGGGACTGACTGGATTTTCATACTTTCTCCTGTTG  
 CTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC  
 ATGGCAATATTGTGAAGAACTGCTGTGAAGTGTGTGTGGCCCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTA  
 TTTTGCCACTGGAGGAAAGTGGAAGTCGACCTCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCC  
 CAGCCCCCACAGAACACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG  
 AGCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACTTTTGTGTTGTGTT  
 TAATTAGGGCTATGAGAGATTTTCAAGTGAGAAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAACT  
 GTTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTGGCATTCTTTCTGCTGCAAGCTTTTTTAAATTTCTGAACT  
 CAAGGCAGTGGCAGAAGATGTCAGTCACCTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCT  
 CCATGGCCTCAGCCACAGGGTCCCCCTTGACCCCCCTCTCTTCCCTCCAGATCCAGCCCTCCTGCTTGGGGTCA  
 TGGTCTCATTCTGGGGCTAAAAGTTTTTGGAGCTGGCTCAAATCCTCCCAAGCTGCTGCACGTGCTGAGTCCAGA  
 GGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTTCTTGGGGTCTTCAGGACTGAAGAGGAGGGAGAG  
 TGGGGTCAAGAGATTCTCCTGGCCACCAAGTGCCAGCATTGCCACAAATCCTTTTAGGAATGGGACAGGTACCT  
 TCCACTTGTGTTANNNNNNNNNNNNNNNNNNNNNNNNNNNNTGTTTTTCTTTTACTCCTGCTCCCATTAGGAG  
 CAGGAATGGCAGTAATAAAAGTCTGCACTTTGGTCATTTCTTTTCTCAGAGGAAGCCCGAGTGCTCACTTAAAC  
 ACTATCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG  
 GCTCTCCTCTCCTCTCCTCTCCCCCGATGTACCCTCAAAAAAAAAAAAAATGCTAACAGTTCTTCCATTAAAGCCT  
 CGGCTGAGTGAGGGAAAGCCAGCACTGCTGCCCTCTCGGGTAACTCACCTAAGGCCTCGGCCACCTCTGGCT  
 ATGTTAACCACACTGGGGGCTTCTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCCAGAGCCACTT  
 CACCTGGGGGTGGGCTGTGGCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTTCAAGGAAGAAGATTTATGT  
 ATTATATGTGGCTATATTTCTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAGGGTCTGTCTGGATGACTTAT  
 CGGTTGGGGGAGTGTAACCGGAACCTTTTCATCTATTTGAAGGCGATTAAACTGTGTCTAATGCA

0997829 101501

## FIGURE 219

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTLFLILGTCTLFFAFECRYLAV  
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP  
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCPWVGNCV GKRNRYFYFL  
FILSLSLLLTIYVFAFNIVYVALKSLKIGFLETCLKETPGTVLEVLI CFFTLWSVVGLTGFHTF  
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVL CGPLPPSVLDRRGILPLEESGSR  
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPEPPQEAAEAEK

### **Putative transmembrane domains:**

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

09978269.10501  
"TOSTOT" 66282660



## FIGURE 220

AAAACCCTGTATTTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT  
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT  
CCCACAGAGCNCTTCGACCATCACTGCCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA  
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA  
ACATCGT

FOST" 15284650

## FIGURE 221

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGACACAAGCTTGAGAGCAACACAA  
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGA  
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC  
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC  
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT  
GACAACCGGGTCAACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA  
CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG  
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC  
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATTTT  
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC  
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC  
GAATACTTGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC  
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATACA  
TTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC  
TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA  
GAAAGGGGTGAAAGTGAAAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTG  
AACATGACTATGGGAACTACACTTGCCTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC  
ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG  
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTTGATGTGAGTGCC  
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC  
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA  
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGAAAAGAGTTTAAAAAAGAAATTGAA  
AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC  
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA  
GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA  
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG  
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA  
AAAAA

## FIGURE 222

MKTIQPKMHNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNR  
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVVDVYDEGPYTCSVQTDNHPK  
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFFVSEDEYL  
EIQGITREQSGDYECASNDVAAPVRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAV  
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNITCVASNKLGHTNASIML  
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLKLF

**Signal peptide:**

amino acids 1-28

09978299 "101501

## FIGURE 223

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC  
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT  
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA  
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT  
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT  
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA  
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATT  
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG  
ACCAGAG

09282650

# FIGURE 224

ATGGCTGGTGACGGCGGGGCGGGCAGGGGACCGGGGCGCGGGCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA  
ATCACCGCCTGGCCCGACTCCACCATGAACGTGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG  
AAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT  
GCACTGCTTCTGGGCTGCCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCACAGCACCTGCCCTTACA  
GAGGCCTGCATTTCAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCTGTGAGGACTTTTAC  
CAGTTCTCCTGTGGGGGTGGATTTCGGAGGAACCCCTGCCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC  
CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAG  
CAGAAGACACAGCGCTTCTACCTATCTTGCCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCAGCCACTGAGA  
GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACCTTTATGGAGGTGTTGAAG  
GCAGTAGCAGGGACCTACAGGGCCACCCATTCTTACCGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGC  
AATGTTATCCAGGTGGACCAGTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG  
AAAGTGCTCACTGCCATATCTGGATTACATGGAGGAAGTGGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG  
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAAACATCACAGTGCCCCAGGACCAGCGGCGCGAC  
GAGGAGAAGATCTACCACAAGATGAGCATTTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC  
CTGTCTTTCTGTCTGTCACCATTTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG  
CAGGTGTCAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG  
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCCTCTATGGCACTAAGAAG  
TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC  
GTGAAGGCCACGTTTGACCGGCAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAG  
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT  
GATATGATTGGTTTCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT  
GAAGATTCTTTCTCCAAAACATGTTGAATTTGTACAACCTTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAG  
CCTCCAGCCGAGACCAGTGGAGCATGACCCCCCAGACAGTGAATGCCTACTACCTTCCAACCTAAGAATGAGATC  
GTCTTCCCGCTGGCATCCTGCAGGCCCCCTTCTATGCCCCGAACCACCCCAAGGCCCTGAACCTTCGGTGGCATC  
GGTGTGGTCATGGGCCATGAGTTGACGCATGCCCCCTTGGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTG  
CGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACACACGGCCTGCATGGAGGAACAGTACAATCAA  
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAG  
GCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC  
AACCACCAGCTCTTCTTCGTGGGATTTGCCAGGTGTGGTGTCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGG  
CTGGTGACCGACCCCCACAGCCCTGCCCCGCTTCCGCGTGTGGGCACTCTCTCCAACCTCCCGTGAATCTCTGCGG  
CACTTCGGCTGCCCTGTGCGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACCTGGATCAGGGGA  
GAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGTTTGTCTCTGGGTGGGAGGAAGCAA  
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACAGGTGACATGAGTACAGACCCCTCCTCAATCACCACATTG  
TGCTCTGCTTTGGGGGTGCCCCCTGCCTCCAGCAGAGCCCCACCATTCACTGTGACATCTTCCGTGTCAACCT  
GCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

097829 "101501

## FIGURE 225

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLLAALLLGCLVALGVQYHRDPSH  
STCLTEACIRVAGKILESIDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQA  
ILKHLLNTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDN  
FMEVLKAVAGTYRATPFFTUYISADSKSSNSNVIQVDQSGFLPSRDYYLNRTANEKVLTA  
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP  
SMDWLEFLSFLLSPLELSDSEPVVVYGM DYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL  
DRRFESAQEKLETLTGKKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI  
SEIRTA FEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF  
FQNMNLNLYNFSKVMADQLRKPPSRDQWSMTPQTVNAYYLPKNEIVFPAGILQAPFYARNH  
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV  
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS  
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNPGLCEVW

**Type II Transmembrane domain:**

amino acids 32-57

09978299.101501  
TDSFOT" 66282660

	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

TTCCCTCCCCTCCCCTCCCCTCCCCTCCCCTCC

## FIGURE 227

GGCCGAGCGGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA  
CCGGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCCGAC  
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG  
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC  
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA  
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTTCGAGTGGCTGGAAAAATCCTGGAGTCCCT  
GGACCGAGGGGTGAGCCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTTCGGA  
GGAACCCCTGCCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC  
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA  
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC  
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG  
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTTCAC  
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG  
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC  
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT  
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTACCTAGTGAACAACTGCCCCCT  
CCTTTCTTTCTTCTTTTCTTCCCTCCCTCCCTTTCTTCCCCTTTTCCTTCCTTCCTTCC  
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTCC  
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTCGATGGGTTCATGGACCT  
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTCAGGAGAGACTTATGGAGCC  
AGCAAAGTCTTCCTGAAGAGATTGCATTTGAGCCAGGTCCTGTAG

09078299-101501



## FIGURE 228

ATGCCTACTACCTTCCAAC TAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC  
TTCTATGCCCCGAACCACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA  
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC  
CCTGGTGGCAGAAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAG  
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT  
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG  
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT  
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGGCTGGTGACCGACCC  
CCACAGCCCTGCCCCGCTTCCGCGTGCTGGGCACTCTCTCCAAC TCCCGTGACTTCCTGCGGC  
ACTTCGGCTGCCCTGTGCGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC  
TGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGT  
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACA  
GGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCT  
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTCACCCTGCCTGGAAGAG  
GTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCCTCTTCTGTCCCCAGGCTCACT  
CAGCCTGGCGGCCATGGGGCCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG  
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCGCACTTAGGGGTGGACTCAGCTCTGTC  
TGGCTCACCTCAGGGGCTACCCCCACCTCACCTGTGCTCCTTGTGCCACTGCTCCCAGTG  
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC  
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTAGCGGGTACTGGTTCCCTGT  
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA  
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT  
TGGCCCTTATAGGACC

09978299 "101501

# FIGURE 229

CCCACGCGTCCGAGCCGCCCCGAGAATTAGACACACTCCGGACGCGGCCAAAAGCAACCGAGA  
 GGAGGGGAGGCAAAAACACCGAAAAACAAAAGAGAGAAACAACACCCAACTGGGGTGG  
 GGGGAAGAAAGAAAAGAAAAGAAACCCACCCACCCACCAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAATCCTGTGGCGCGCCGCTGGTTCCCGGGAAGACTCGCCAGCACCAGGGGG  
 TGGGGGAGTGCGAGCTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGACATGATG  
 CTGTTGGTGCAGGGTGCTTGTGCTCGAACCAGTGGCTGGCGCGGTGCTCCTCAGCCTGTG  
 CTGCCTGCTACCCCTCCTGCCTCCCGGCTGGACAGAGTGTGGACTTCCCCTGGGCGGCCGTGG  
 ACAACATGATGGTGCAGAAAAGGGGACACGGCGGTGCTTAGGTGTTATTTTGAAGATGGAGCT  
 TCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTATTTTTGCGGGAGGTGATAAGTGGTCAGT  
 GGATCCTCGAGTTTCAATTTCAACATTGAATAAAAGGGACTACAGCCTCCAGATACAGAATG  
 TAGATGTGACAGATGATGGCCCATACACGTGTTCTGTTTCAAGTCAACATACACCCAGAAC  
 ATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC  
 CGTCAATGAAGGAACCAACGTCACTCTTACTTGTGTTGGCCACTGGGAAACCAGAGCCTTCCA  
 TTTCTTGGCGACACATCTCCCATCAGCAAAACCATTTGAAAATGGACAATATTTGGACATT  
 TATGGAATTACAAGGGACCAGGCTGGGGAATATGAATGCAGTGCGGAAAATGCTGTGTGATT  
 CCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACTTTGCTCCTACTATTCAGGAAATTAAT  
 CTGGCACCGTGACCCCCGGACGCAGTGGCCTGATAAGATGTGAAGGTGCAGGTGTGCCGCT  
 CCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCTCTTCAATGGCCAACAAGGAATTATTAT  
 TCAAAATTTTAGCACAAAGATCCATTCTCACTGTTACCAACGTGACACAGGAGCACTTCGGCA  
 ATTATACCTGTGTGGCTGCCAACAAGCTAGGCACAACCAATGCGAGCCTGCCTCTTAACCT  
 CCAAGTACAGCCCAGTATGGAATTACCGGGAGCGCTGATGTTCTTTCTCCTGCTGGTACCT  
 TGTGTTGACACTGTCTCTTTCACCAGCATATTCTACCTGAAGAATGCCATTCTACAATAAA  
 TTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCTGAAAGTGCTGATGGCTGGATCCAATCT  
 GGTACAGTTTGTGTTAAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGGATGATCGCC  
 TTCTGTAGAATTGCTCATTATGTAAATACTTTAATTCTACTCTTTTTTGATTAGCTACATTA  
 CCTTGTGAAGCAGTACACATTGTCTTTTTTAAGACGTGAAAGCTCTGAAATTACTTTTAG  
 AGGATATTAATTGTGATTTCATGTTTGTAACTTCTACAACTTTTCAAAGCATTCAATCATGGT  
 CTGCTAGGTTGCAGGCTGTGTTTACAAACGAATATTGCAGTGAATATGTGATTCTTTAA  
 GGCTGCAATAACAAGCATTCACTTCCCTGTTTCAATAAGAGTCAATCCACATTACAAAGATG  
 CATTTTTTTCTTTTTTGATAAAAAAGCAATAATTGCCTTCAGATTATTTCTTCAAATA  
 TAACACATATCTAGATTTTTCTGCTTGCATGATATTCAAGTTTCAGGAATGAGCCTTGTAA  
 ATAAGTGGCTGTGCAGCTCTGCTTCTCTTTCCTGTAAGTTTCAGCATGGGTGTGCCTTCATAC  
 AATAATATTTTTCTCTTTGTCTCCAACATAATATAAAATGTTTTGCTAAATCTTACAATTTGA  
 AAGTAAAAATAAACCAGAGTGATCAAGTTAAACCATACACTATCTCTAAGTAACGAAGGAGC  
 TATTGGACTGTAAAAATCTCTTCTGCACTGACAATGGGGTTTGAGAATTTTGCCCCACACT  
 AACTCAGTTCTTGTGATGAGAGACAATTTAATAACAGTATAGTAAATATACCATATGATTTCT  
 TTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGAAATCATTCCCTTTAAAATGACAGCACA  
 GTCCACTCAAAGGATTGCCTAGCAATACAGCATCTTTTCCTTTCACTAGTCCAAGCCAAAAA  
 TTTTAAGATGATTTGTGAGAAAGGGCACAAAGTCCTATCACCTAATATTACAAGAGTTGGTA  
 AGCGCTCATCATTAATTTTATTTTGTGGCAGGTATTATGACAGTCGACCTGGAGGGTATGGA  
 TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACCAGGGTGGTTATGACCGCTACTC  
 AGGAGGAAATTACAGAGACAATTATGACAACTGAAATGAGACATGCACATAATATAGATACA  
 CAAGGAATAATTTCTGATCCAGGATCGTCCTTCAAATGGCTGTATTTATAAAGGTTTTTGG  
 AGCTGCACTGAAGCATCTTATTTTATAGTATATCAACCTTTTGTTTTTTAAATTGACCTGCCA  
 AGGTAGCTGAAGACCTTTTAGACAGTTCCATCTTTTTTTTTTAAATTTTTCTGCCTATTTAA  
 AGACAAATTATGGGACGTTTGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

0973299.101501

## **FIGURE 230**

MMLLVQGACCSNQWLA AVL LLSL CCLLP SCLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYLED  
GASKGAWLNRSSII FAGGDKWSVDPRVSISTLNKRDYSLQIQNV DVTDDGPYTCSVQTQHTP  
RTMQVHLTVQVPPKIYDISNDMTVNEGTVNTLTCLATGKPEPSISWRHISPSAKPFENGQYL  
DIYGITRDQAGEYECSAENAVSFDPVRKVKV VVNFAPT IQEIKSGTVTPGRSGLIRCEGAGV  
PPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASLPL  
NPPSTAQYGITGSADVLFSCWYLVLTLS SFTSIFYLKNAILQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 326-345

#### **N-glycosylation sites.**

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

#### **Casein kinase II phosphorylation site.**

amino acids 147-151, 208-212, 224-228

#### **Tyrosine kinase phosphorylation site.**

amino acids 178-186

#### **N-myristoylation sites.**

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,  
302-308, 319-325

#### **Myelin P0 protein:**

amino acids 92-121

0978299-10504  
TOSTOT " 56287660

## FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTTCTGCTGG  
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGA  
CGAGCTCTTGAGTGAGACCCAACAAGCTGCTTTTCACCAAATTGCAATGGAGCCTTTTCGAAA  
TCAATGTTCCAAAGCCCCAAGAGGAGAAATGGGGTGAACCTTCTCCCTAGCTGTGGTGGTCATC  
TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC  
GCGGCTCCGGGTCTTGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT  
CCTTCTCCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTG  
CAAGTCCTGCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGT  
AGACAACTTCACTCAGAACCCAGGGATGTTTCAAGATCAAAGGTGAACAAGGCGCCCCAGGTC  
TTCAAGGTCAACAAGGGGGCCATGGGCATGCCTGGTGCCCCCTGGCCCCGCCGGGACCACCTGCT  
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCCCTCGGGACCCCAAGG  
CCCACCGGGAGTCAAGGGAGAGGCGGGCCTCCAAGGACCCCAAGGTGCTCCAGGGAAGCAAG  
GAGCCACTGGCACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATT  
GGCCCAAAAGGGGAACTGGAACCTAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA  
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTGAGGGCCTCCTGGAGCCCAGGGGAGTA  
AAGGTGACTTCGGGAGGCCAGGCCCACAGGTTTGGCTGGTTTTCTGGAGCTAAAGGAGAT  
CAAGGACAACCTGGACTGCAGGGTGTTCGCGGCCCTCCTGGTGCAGTGGGACACCCAGGTGC  
CAAGGTGAGCCTGGCAGTGTCTGGCTCCCCTGGGCGAGCAGGACTTCAGGGAGCCCCGGGA  
GTCCAGGAGCCACAGGCCTGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGA  
AGAAAAGGAGAATCAGGAGTTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGG  
GCTGGCAGGTCCCAAGGGAGCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG  
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAAGGTGAAAGAGGTGAAAACTCAGTGTCC  
GTCAGGATTGTGCGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG  
GACAATTTGCGATGACGAGTGGCAAAATTCTGATGCCATTGTCTTCTGCCGCATGCTGGGTT  
ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT  
GTTTCAAGTGTGCGGGCACGGAGAGTACCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCA  
TGAATGCAGCCACGAGGAGGACGCAGGCGTGGAGTGCAGCGTCTGAACCCGAAACCCCTTTCA  
CTTCTCTGCTCCCGAGGTGTCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT  
TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTAATAAAGCTCAACATCATTGA

## FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAFHQIAMEPF EINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL  
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVR  
VSHEHLLQRVDNFTQNP GFMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRD  
GATGPSGPQGP PGVKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGE  
KGD LGLPGSKGDRGMKGDAGVMGPPGAQGSKGD FGRPGPPGLAGFP GAKGDQGPGLQGVPG  
PPGAVGHPPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKGSKGD TGLQGGQGRKGESGVPGPA  
GVKGEQGS PGLAGPKGAPGQAGQKGDQGVKGSSGEQGVKGEKGERGENSVSVRIVGSSNRGR  
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWL DNVQCRGTESTLW  
SCTKNSWGHHDCSHEEDAGVECSV

### **Transmembrane domain:**

amino acids 47-66 (type II)

### **N-glycosylation sites.**

amino acids 43-47, 83-87, 136-140

### **Tyrosine kinase phosphorylation site.**

amino acids 432-440

### **N-myristoylation sites.**

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,  
400-406, 441-447, 475-481, 490-496, 515-521

### **Amidation site.**

amino acids 360-364

### **Leucine zipper pattern.**

amino acids 56-78

### **Speract receptor repeat**

amino acids 422-471, 488-519

### **Clq domain proteins.**

amino acids 151-184, 301-334, 316-349

09978299 101501  
TOSTOT "65282660

## FIGURE 233

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT  
CTTCTCCTTTTGCCCAAACACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG  
ACCAAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTTTTAC  
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA  
GAAAGATACTAAAAGATCACAACTGTCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG  
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTACTG  
CAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACCAAAGATCTCTTTTCG  
TGATTCTTGCAACAATCAATGAGAATCTTCATGTATTCTGGAGAACACCATTCCTGATTTT  
CCACAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT  
AGATTCTATAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA  
AGTTAATTCAATCTAAAAAAAAAAAAA

09978299-101501

## FIGURE 234

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758

<subunit 1 of 1, 98 aa, 1 stop

<MW: 11081, pI: 6.68, NX(S/T): 1

MKLMVLVFTIGLTLLLG VQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDG  
KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **N-glycosylation site.**

amino acids 72-76

#### **Tyrosine kinase phosphorylation site.**

amino acids 63-71

09078299-101501  
TOSTOT" 56282660

# FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGTCTGGAGCGAATTCCAGCCTGCAGGG  
 CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCCGCCGTGGTGGTTGGAGGGC  
 GCGCAGTAGAGCAGCAGCACAGGCGCGGGTCCCGGGAGGCGCGCTCTGCTCGCGCCGAGATG  
 TGGAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACCGCGCGCCGCCGCGCTGGCTGTG  
 CGCTGGGGCGCTGGTGCTGGCGGGTGGCTTCTTCTCCTCGGCTTCTCTTTCGGGTGGTTTA  
 TAAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTGGAT  
 GAATTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGC  
 AGGAACAGAACAAAACCTTTCAGCTTGCAAAGCAAATTCATCCCAGTGGAAAGAATTTGGCC  
 TGGATTCTGTTGAGCTAGCTCATTATGATGTCCTGTTGTCTTACCCAAATAAGACTCATCCC  
 AACTACATCTCAATAATTAATGAAGATGGAAATGAGATTTTCAACACATCATTATTTGAACC  
 ACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACCTTTCAGTGCTTCTCTCCTC  
 AAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAACTGAAGACTTCTTTAAA  
 TTGGAACGGGACATGAAAATCAATTGCTCTGGGAAAATTGTAATTGCCAGATATGGGAAAGT  
 TTTTCAGAGGAAATAAGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACT  
 CCGACCCTGCTGACTACTTTGCTCCTGGGGTGAAGTCCTATCCAGACGGTTGGAATCTTCCT  
 GGAGGTGGTGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACC  
 AGGTTACCCAGCAAATGAATATGCTTATAGGCGTGGAAATTCAGAGGCTGTTGGTCTTCCAA  
 GTATTCCTGTTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGC  
 TCAGCACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG  
 CTTTACTGGAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA  
 CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGATATGTCATT  
 CTGGGAGGTCAACGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAGCTGT  
 TGTTTCATGAAATTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGAA  
 CAATTTTGTTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTGAGTGGGCA  
 GAGGAGAATTCAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT  
 AGAAGGAAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACACAACC  
 TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATGAAAGTTGG  
 ACTAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCAGGATAAGCAAATTTGGGATCTGG  
 AAATGATTTTGGAGGTGTTCTTCCAACGACTTGGAATTGCTTCAGGCAGAGCACGGTATACTA  
 AAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATAT  
 GAGTTGGTGGAAAAGTTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCAGGTTTCG  
 AGGAGGGATGGTGTGTTGAGCTAGCCAATTCATAGTGCTCCCTTTTGTATTGTCGAGATTATG  
 CTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAA  
 ATGAAGACATACAGTGTATCATTGATTCACTTTTTTCTGCAGTAAAGAATTTTACAGAAAT  
 TGCTTCCAAGTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATAGTATTAAGAA  
 TGATGAATGATCAACTCATGTTTCTGGAAAGAGCATTTATTGATCCATTAGGGTTACCAGAC  
 AGGCCTTTTTATAGGCATGTCATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTC  
 ATTCCCAGGAATTTATGATGCTCTGTTTGTATTTGAAAGCAAAGTGGACCCTTCCAAGGCCT  
 GGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCACAGTGCAGGCAGCTGCAGAGACT  
 TTGAGTGAAGTAGCCTAAGAGGATTTTTTAGAGAATCCGTATTGAATTTGTGTGGTATGTCA  
 CTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAAATTGGTATATTTGAAATAAAGT  
 TGAATATTATATATAA

09978299-101504



Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	Male	Female		
Marital status	Married	Single		
Education	High school	College		
Occupation	Manager	Worker		
Income	Low	High		
Health status	Good	Poor		
Stress level	Low	High		
Life satisfaction	High	Low		
Resilience	High	Low		
Optimism	High	Low		
Self-efficacy	High	Low		
Perceived social support	High	Low		
Perceived stress	Low	High		
Depression	Low	High		
Anxiety	Low	High		
Quality of life	High	Low		
Life expectancy	High	Low		
Healthcare utilization	High	Low		
Health insurance	Yes	No		
Healthcare access	Good	Poor		
Healthcare quality	High	Low		
Healthcare cost	Low	High		
Healthcare satisfaction	High	Low		
Healthcare utilization	High	Low		
Healthcare access	Good	Poor		
Healthcare quality	High	Low		
Healthcare cost	Low	High		
Healthcare satisfaction	High	Low		

><MW: 84305, pI: 6.93, NX(S/T): 10

amino acids 1-40

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,  
459-463, 476-480, 638-642

amino acids 363-372, 605-613, 606-613, 617-626

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,  
360-366, 427-433, 529-535, 707-713